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FIG. 1A TECH CENTER 1600/2300

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	CLASS	

CTG CTC GCC GCC GTG GAA GAA ACG CTA ATG GAC TCC ACT ACA GCG ACT Leu Leu Ala Ala Val Glu Glu Thr Leu Met Asp Ser Thr Thr Ala Thr 1 5 10 15	48
GCT GAG CTG GGC TGG ATG GTG CAT CCT CCA TCA GGG TGG GAA GAG GTG Ala Glu Leu Gly Trp Met Val His Pro Pro Ser Gly Trp Glu Glu Val 20 25 30	96
AGT GGC TAC GAT GAG AAC ATG AAC ACG ATC CGC ACG TAC CAG GTG TGC Ser Gly Tyr Asp Glu Asn Met Asn Thr Ile Arg Thr Tyr Gln Val Cys 35 40 45	144
AAC GTG TTT GAG TCA AGC CAG AAC AAC TGG CTA CGG ACC AAG TTT ATC Asn Val Phe Glu Ser Ser Gln Asn Asn Trp Leu Arg Thr Lys Phe Ile 50 55 60	192
CGG CGC CGT GGG GCC CAC CGC ATC CAC GTG GAG ATG AAG TTT TCG GTG Arg Arg Arg Gly Ala His Arg Ile His Val Glu Met Lys Phe Ser Val 65 70 75 80	240
CGT GAC TGC AGC AGC ATC CCC AGC GTG CCT GGC TCC TGC AAG GAG ACC Arg Asp Cys Ser Ser Ile Pro Ser Val Pro Gly Ser Cys Lys Glu Thr 85 90 95	288
TTC AAC CTC TAT TAC TAT GAG GCT GAC TTT GAC TCG GCC ACC AAG ACC Phe Asn Leu Tyr Tyr Tyr Glu Ala Asp Phe Asp Ser Ala Thr Lys Thr 100 105 110	336
TTC CCC AAC TGG ATG GAG AAT CCA TGG GTG AAG GTG GAT ACC ATT GCA Phe Pro Asn Trp Met Glu Asn Pro Trp Val Lys Val Asp Thr Ile Ala 115 120 125	384
GCC GAC GAG AGC TTC TCC CAG GTG GAC CTG GGT GGC CGC GTC ATG AAA Ala Asp Glu Ser Phe Ser Gln Val Asp Leu Gly Gly Arg Val Met Lys 130 135 140	432
ATC AAC ACC GAG GTG CGG AGC TTC GGA CCT GTG TCC CGC AGC GGC TTC Ile Asn Thr Glu Val Arg Ser Phe Gly Pro Val Ser Arg Ser Gly Phe 145 150 155 160	480
TAC CTG GCC TTC CAG GAC TAT GGC GGC TGC ATG TCC CTC ATC GCC GTG Tyr Leu Ala Phe Gln Asp Tyr Gly Gly Cys Met Ser Leu Ile Ala Val 165 170 175	528
CGT GTC TTC TAC CGC AAG TGC CCC CGC ATC ATC CAG AAT GGC GCC ATC Arg Val Phe Tyr Arg Lys Cys Pro Arg Ile Ile Gln Asn Gly Ala Ile 180 185 190	576



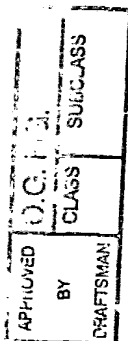
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FIG. 1B

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TTC	CAG	GAA	ACC	CTG	TCG	GGG	GCT	GAG	AGC	ACA	TCG	CTG	GTG	GCT	GCC	624
Phe	Gln	Glu	Thr	Leu	Ser	Gly	Ala	Glu	Ser	Thr	Ser	Leu	Val	Ala	Ala	
		195					200					205				
CGG	GGC	AGC	TGC	ATC	GCC	AAT	GCG	GAA	GAG	GTG	GAT	GTA	CCC	ATC	AAG	672
Arg	Gly	Ser	Cys	Ile	Ala	Asn	Ala	Glu	Glu	Val	Asp	Val	Pro	Ile	Lys	
	210					215					220					
CTC	TAC	TGT	AAC	GGG	GAC	GGC	GAG	TGG	CTG	GTG	CCC	ATC	GGG	CGC	TGC	720
Leu	Tyr	Cys	Asn	Gly	Asp	Gly	Glu	Trp	Leu	Val	Pro	Ile	Gly	Arg	Cys	
	225				230					235					240	
ATG	TGC	AAA	GCA	GGC	TTC	GAG	GCC	GTT	GAG	AAT	GGC	ACC	GTC	TGC	CGA	768
Met	Cys	Lys	Ala	Gly	Phe	Glu	Ala	Val	Glu	Asn	Gly	Thr	Val	Cys	Arg	
				245					250					255		
GGT	TGT	CCA	TCT	GGG	ACT	TTC	AAG	GCC	AAC	CAA	GGG	GAT	GAG	GCC	TGT	816
Gly	Cys	Pro	Ser	Gly	Thr	Phe	Lys	Ala	Asn	Gln	Gly	Asp	Glu	Ala	Cys	
			260					265					270			
ACC	CAC	TGT	CCC	ATC	AAC	AGC	CGG	ACC	ACT	TCT	GAA	GGG	GCC	ACC	AAC	864
Thr	His	Cys	Pro	Ile	Asn	Ser	Arg	Thr	Thr	Ser	Glu	Gly	Ala	Thr	Asn	
		275					280					285				
TGT	GTC	TGC	CGC	AAT	GGC	TAC	TAC	AGA	GCA	GAC	CTG	GAC	CCC	CTG	GAC	912
Cys	Val	Cys	Arg	Asn	Gly	Tyr	Tyr	Arg	Ala	Asp	Leu	Asp	Pro	Leu	Asp	
	290					295					300					
ATG	CCC	TGC	ACA	ACC	ATC	CCC	TCC	GCG	CCC	CAG	GCT	GTG	ATT	TCC	AGT	960
Met	Pro	Cys	Thr	Thr	Ile	Pro	Ser	Ala	Pro	Gln	Ala	Val	Ile	Ser	Ser	
	305				310					315					320	
GTC	AAT	GAG	ACC	TCC	CTC	ATG	CTG	GAG	TGG	ACC	CCT	CCC	CGC	GAC	TCC	1008
Val	Asn	Glu	Thr	Ser	Leu	Met	Leu	Glu	Trp	Thr	Pro	Pro	Arg	Asp	Ser	
				325				330						335		
GGA	GGC	CGA	GAG	GAC	CTC	GTC	TAC	AAC	ATC	ATC	TGC	AAG	AGC	TGT	GGC	1056
Gly	Gly	Arg	Glu	Asp	Leu	Val	Tyr	Asn	Ile	Ile	Cys	Lys	Ser	Cys	Gly	
			340					345					350			
TCG	GGC	CGG	GGT	GCC	TGC	ACC	CGC	TGC	GGG	GAC	AAT	GTA	CAG	TAC	GCA	1104
Ser	Gly	Arg	Gly	Ala	Cys	Thr	Arg	Cys	Gly	Asp	Asn	Val	Gln	Tyr	Ala	
		355					360					365				
CCA	CGC	CAG	CTA	GGC	CTG	ACC	GAG	CCA	CGC	ATT	TAC	ATC	AGT	GAC	CTG	1152
Pro	Arg	Gln	Leu	Gly	Leu	Thr	Glu	Pro	Arg	Ile	Tyr	Ile	Ser	Asp	Leu	
		370				375					380					
CTG	GCC	CAC	ACC	CAG	TAC	ACC	TTC	GAG	ATC	CAG	GCT	GTG	AAC	GGC	GTT	1200
Leu	Ala	His	Thr	Gln	Tyr	Thr	Phe	Glu	Ile	Gln	Ala	Val	Asn	Gly	Val	
					390					395					400	





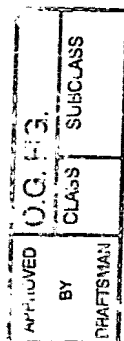
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FIG. 1C

ACT GAC CAG AGC CCC TTC TCG CCT CAG TTC GCC TCT GTG AAC ATC ACC	1248
Thr Asp Gln Ser Pro Phe Ser Pro Gln Phe Ala Ser Val Asn Ile Thr	
405 410 415	
ACC AAC CAG GCA GCT CCA TCG GCA GTG TCC ATC ATG CAT CAG GTG AGC	1296
Thr Asn Gln Ala Ala Pro Ser Ala Val Ser Ile Met His Gln Val Ser	
420 425 430	
CGC ACC GTG GAC AGC ATT ACC CTG TCG TGG TCC CAG CCG GAC CAG CCC	1344
Arg Thr Val Asp Ser Ile Thr Leu Ser Trp Ser Gln Pro Asp Gln Pro	
435 440 445	
AAT GGC GTG ATC CTG GAC TAT GAG CTG CAG TAC TAT GAG AAG GAG CTC	1392
Asn Gly Val Ile Leu Asp Tyr Glu Leu Gln Tyr Tyr Glu Lys Glu Leu	
450 455 460	
AGT GAG TAC AAC GCC ACA GCC ATA AAA AGC CCC ACC AAC ACG GTC ACG	1440
Ser Glu Tyr Asn Ala Thr Ala Ile Lys Ser Pro Thr Asn Thr Val Thr	
465 470 475 480	
GGC CTC AAA GCC GGC GCC ATC TAT GTC TTC CAG GTG CGG GCA CGC ACT	1488
Gly Leu Lys Ala Gly Ala Ile Tyr Val Phe Gln Val Arg Ala Arg Thr	
485 490 495	
GTG GCA GGC TAC GGG CGC TAC AGC GGC AAG ATG TAC TTC CAG ACC ATG	1536
Val Ala Gly Tyr Gly Arg Tyr Ser Gly Lys Met Tyr Phe Gln Thr Met	
500 505 510	
ACA GAA GCC GAG TAC CAG ACA AGC ATC CAG GAG AAG TTG CCA CTC ATC	1584
Thr Glu Ala Glu Tyr Gln Thr Ser Ile Gln Glu Lys Leu Pro Leu Ile	
515 520 525	
ATC GGC TCC TCG GCC GCT GGC CTG GTC TTC CTC ATT GCT GTG GTT GTC	1632
Ile Gly Ser Ser Ala Ala Gly Leu Val Phe Leu Ile Ala Val Val Val	
530 535 540	
ATC GCC ATC GTG TGT AAC AGA CGG GGG TTT GAG CGT GCT GAC TCG GAG	1680
Ile Ala Ile Val Cys Asn Arg Arg Gly Phe Glu Arg Ala Asp Ser Glu	
545 550 555 560	
TAC ACG GAC AAG CTG CAA CAC TAC ACC AGT GGC CAC ATA ACC CCA GGC	1728
Tyr Thr Asp Lys Leu Gln His Tyr Thr Ser Gly His Ile Thr Pro Gly	
565 570 575	
ATG AAG ATC TAC ATC GAT CCT TTC ACC TAC GAG GAC CCC AAC GAG GCA	1776
Met Lys Ile Tyr Ile Asp Pro Phe Thr Tyr Glu Asp Pro Asn Glu Ala	
580 585 590	
GTG CGG GAG TTT GCC AAG GAA ATT GAC ATC TCC TGT GTC AAA ATT GAG	1824
Val Arg Glu Phe Ala Lys Glu Ile Asp Ile Ser Cys Val Lys Ile Glu	
595 600 605	





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FIG. 1D

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CAG GTG ATC GGA GCA GGG GAG TTT GGC GAG GTC TGC AGT GGC CAC CTG 1872  
Gln Val Ile Gly Ala Gly Glu Phe Gly Glu Val Cys Ser Gly His Leu  
610 615 620

AAG CTG CCA GGC AAG AGA GAG ATC TTT GTG GCC ATC AAG ACG CTC AAG 1920  
Lys Leu Pro Gly Lys Arg Glu Ile Phe Val Ala Ile Lys Thr Leu Lys  
625 630 635 640

TCG GGC TAC ACG GAG AAG CAG CGC CGG GAC TTC CTG AGC GAA GCC TCC 1968  
Ser Gly Tyr Thr Glu Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser  
645 650 655

ATC ATG GGC CAG TTC GAC CAT CCC AAC GTC ATC CAC CTG GAG GGT GTC 2016  
Ile Met Gly Gln Phe Asp His Pro Asn Val Ile His Leu Glu Gly Val  
660 665 670

GTG ACC AAG AGC ACA CCT GTG ATG ATC ATC ACC GAG TTC ATG GAG AAT 2064  
Val Thr Lys Ser Thr Pro Val Met Ile Ile Thr Glu Phe Met Glu Asn  
675 680 685

GGC TCC CTG GAC TCC TTT CTC CGG CAA AAC GAT GGG CAG TTC ACA GTC 2112  
Gly Ser Leu Asp Ser Phe Leu Arg Gln Asn Asp Gly Gln Phe Thr Val  
690 695 700

ATC CAG CTG GTG GGC ATG CTT CGG GGC ATC GCA GCT GGC ATG AAG TAC 2160  
Ile Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr  
705 710 715 720

CTG GCA GAC ATG AAC TAT GTT CAC CGT GAC CTG GCT GCC CGC AAC ATC 2208  
Leu Ala Asp Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile  
725 730 735

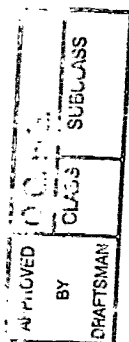
CTC GTC AAC AGC AAC CTG GTC TGC AAG GTG TCG GAC TTT GGG CTC TCA 2256  
Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser  
740 745 750

CGC TTT CTA GAG GAC GAT ACC TCA GAC CCC ACC TAC ACC AGT GCC CTG 2304  
Arg Phe Leu Glu Asp Asp Thr Ser Asp Pro Thr Tyr Thr Ser Ala Leu  
755 760 765

GGC GGA AAG TTC CCC ATC CGC TGG ACA GCC CCG GAA GCC ATC CAG TAC 2352  
Gly Gly Lys Phe Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Gln Tyr  
770 775 780

CGG AAG TTC ACC TCG GCC AGT GAT GTG TGG AGC TAC GGC ATT GTC ATG 2400  
Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met  
785 790 795 800

TGG GAG GTG ATG TCC TAT GGG GAG CGG CCC TAC TGG GAC ATG ACC AAC 2448  
Trp Glu Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Thr Asn  
805 810 815





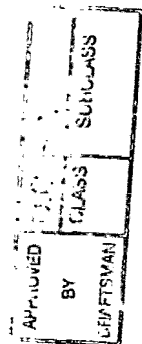
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FIG. 1E

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CAG GAT GTA ATC AAT GCC ATT GAG CAG GAC TAT CGG CTG CCA CCG CCC	2496
Gln Asp Val Ile Asn Ala Ile Glu Gln Asp Tyr Arg Leu Pro Pro Pro	
20 825 830	
ATG GAC TGC CCG AGC GCC CTG CAC CAA CTC ATG CTG GAC TGT TGG CAG	2544
Met Asp Cys Pro Ser Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln	
835 840 845	
AAG GAC CGC AAC CAC CGG CCC AAG TTC GGC CAA ATT GTC AAC ACG CTA	2592
Lys Asp Arg Asn His Arg Pro Lys Phe Gly Gln Ile Val Asn Thr Leu	
850 855 860	
GAC AAG ATG ATC CGC AAT CCC AAC AGC CTC AAA GCC ATG GCG CCC CTC	2640
Asp Lys Met Ile Arg Asn Pro Asn Ser Leu Lys Ala Met Ala Pro Leu	
865 870 875 880	
TCC TCT GGC ATC AAC CTG CCG CTG CTG GAC CGC ACG ATC CCC GAC TAC	2688
Ser Ser Gly Ile Asn Leu Pro Leu Leu Asp Arg Thr Ile Pro Asp Tyr	
885 890 895	
ACC AGC TTT AAC ACG GTG GAC GAG TGG CTG GAG GCC ATC AAG ATG GGG	2736
Thr Ser Phe Asn Thr Val Asp Glu Trp Leu Glu Ala Ile Lys Met Gly	
900 905 910	
CAG TAC AAG GAG AGC TTC GCC AAT GCC GGC TTC ACC TCC TTT GAC GTC	2784
Gln Tyr Lys Glu Ser Phe Ala Asn Ala Gly Phe Thr Ser Phe Asp Val	
915 920 925	
GTG TCT CAG ATG ATG ATG GAG GAC ATT CTC CGG GTT GGG GTC ACT TTG	2832
Val Ser Gln Met Met Met Glu Asp Ile Leu Arg Val Gly Val Thr Leu	
930 935 940	
GCT GGC CAC CAG AAA AAA ATC CTG AAC AGT ATC CAG GTG ATG CCG GCG	2880
Ala Gly His Gln Lys Lys Ile Leu Asn Ser Ile Gln Val Met Arg Ala	
945 950 955 960	
CAG ATG AAC CAG ATT CAG TCT GTG GAG GTT TGACATTCAC CTGCCTCGGC	2930
Gln Met Asn Gln Ile Gln Ser Val Glu Val	
965 970	
TCACCTCTTC CTCCAAGCCC CGCCCCCTCT GC	2962





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## FIG. 2A

CCA	GCG	TCC	CTG	GCC	GGC	TGC	TAC	TCT	GCA	CCT	CGA	CGG	GCT	CCC	CTC	48
Pro	Ala	Ser	Leu	Ala	Gly	Cys	Tyr	Ser	Ala	Pro	Arg	Arg	Ala	Pro	Leu	
1				5					10					15		
TGG	ACG	TGC	CTT	CTC	CTG	TGC	GCC	GCA	CTC	CGG	ACC	CTC	CTG	GCC	AGC	96
Trp	Thr	Cys	Leu	Leu	Leu	Cys	Ala	Ala	Leu	Arg	Thr	Leu	Leu	Ala	Ser	
			20					25					30			
CCC	AGC	AAC	GAA	GTG	AAT	TTA	TTG	GAT	TCA	CGC	ACT	GTC	ATG	GGG	GAC	144
Pro	Ser	Asn	Glu	Val	Asn	Leu	Leu	Asp	Ser	Arg	Thr	Val	Met	Gly	Asp	
		35					40					45				
CTG	GGA	TGG	ATT	GCT	TTT	CCA	AAA	AAT	GGG	TGG	GAA	GAG	ATT	GGT	GAA	192
Leu	Gly	Trp	Ile	Ala	Phe	Pro	Lys	Asn	Gly	Trp	Glu	Glu	Ile	Gly	Glu	
	50					55					60					
GTG	GAT	GAA	AAT	TAT	GCC	CCT	ATC	CAC	ACA	TAC	CAA	GTA	TGC	AAA	GTG	240
Val	Asp	Glu	Asn	Tyr	Ala	Pro	Ile	His	Thr	Tyr	Gln	Val	Cys	Lys	Val	
	65				70					75					80	
ATG	GAA	CAG	AAT	CAG	AAT	AAC	TGG	CTT	TTG	ACC	AGT	TGG	ATC	TCC	AAT	288
Met	Glu	Gln	Asn	Gln	Asn	Asn	Trp	Leu	Leu	Thr	Ser	Trp	Ile	Ser	Asn	
				85					90					95		
GAA	GGT	GCT	TCC	AGA	ATC	TTC	ATA	GAA	CTC	AAA	TTT	ACC	CTG	CGG	GAC	336
Glu	Gly	Ala	Ser	Arg	Ile	Phe	Ile	Glu	Leu	Lys	Phe	Thr	Leu	Arg	Asp	
			100					105					110			
TGC	AAC	AGC	CTT	CCT	GGA	GGA	CTG	GGG	ACC	TGT	AAG	GAA	ACC	TTT	AAT	384
Cys	Asn	Ser	Leu	Pro	Gly	Gly	Leu	Gly	Thr	Cys	Lys	Glu	Thr	Phe	Asn	
		115					120					125				
ATG	TAT	TAC	TTT	GAG	TCA	GAT	GAT	CAG	AAT	GGG	AGA	AAC	ATC	AAG	GAA	432
Met	Tyr	Tyr	Phe	Glu	Ser	Asp	Asp	Gln	Asn	Gly	Arg	Asn	Ile	Lys	Glu	
	130					135					140					
AAC	CAA	TAC	ATC	AAA	ATT	GAT	ACC	ATT	GCT	GCC	GAT	GAA	AGC	TTT	ACA	480
Asn	Gln	Tyr	Ile	Lys	Ile	Asp	Thr	Ile	Ala	Ala	Asp	Glu	Ser	Phe	Thr	
	145				150					155					160	
GAA	CTT	GAT	CTT	GGT	GAC	CGT	GTT	ATG	AAA	CTG	AAT	ACA	GAG	GTC	AGA	528
Glu	Leu	Asp	Leu	Gly	Asp	Arg	Val	Met	Lys	Leu	Asn	Thr	Glu	Val	Arg	
				165					170					175		
GAT	GTA	GGA	CCT	CTA	AGC	AAA	AAG	GGA	TTT	TAT	CTT	GCT	TTT	CAA	GAT	576
Asp	Val	Gly	Pro	Leu	Ser	Lys	Lys	Gly	Phe	Tyr	Leu	Ala	Phe	Gln	Asp	
			180					185					190			
GTT	GGT	GCT	TGC	ATT	GCT	CTG	GTT	TCT	GTG	CGT	GTA	TAC	TAT	AAA	AAA	624
Val	Gly	Ala	Cys	Ile	Ala	Leu	Val	Ser	Val	Arg	Val	Tyr	Tyr	Lys	Lys	
		195					200					205				

O.G. FIG.	SUBCLASS
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## FIG. 2B

TGC	CCT	TCT	GTG	GTA	CGA	CAC	TTG	GCT	GTC	TTC	CCT	GAC	ACC	ATC	ACT		
Cys	Pro	Ser	Val	Val	Arg	His	Leu	Ala	Val	Phe	Pro	Asp	Thr	Ile	Thr		
210						215					220						
GGA	GCT	GAT	TCT	TCC	CAA	TTG	CTC	GAA	GTG	TCG	GGC	TCC	TGT	GTC	AAC		720
Gly	Ala	Asp	Ser	Ser	Gln	Leu	Leu	Glu	Val	Ser	Gly	Ser	Cys	Val	Asn		
225					230					235					240		
CAT	TCT	GTG	ACC	GAT	GAA	CCT	CCC	AAA	ATG	CAC	TGC	AGC	GCC	GAA	GGG		768
His	Ser	Val	Thr	Asp	Glu	Pro	Pro	Lys	Met	His	Cys	Ser	Ala	Glu	Gly		
				245					250					255			
GAG	TGG	CTG	GTG	CCC	ATC	GGG	AAA	TGC	ATG	TGC	AAG	GCA	GGA	TAT	GAA		816
Glu	Trp	Leu	Val	Pro	Ile	Gly	Lys	Cys	Met	Cys	Lys	Ala	Gly	Tyr	Glu		
			260					265					270				
GAG	AAA	AAT	GGC	ACC	TGT	CAA	GTG	TGC	AGA	CCT	GGG	TTC	TTC	AAA	GCC		864
Glu	Lys	Asn	Gly	Thr	Cys	Gln	Val	Cys	Arg	Pro	Gly	Phe	Phe	Lys	Ala		
		275						280				285					
TCA	CCT	CAC	ATC	CAG	AGC	TGC	GGC	AAA	TGT	CCA	CCT	CAC	AGT	TAT	ACC		912
Ser	Pro	His	Ile	Gln	Ser	Cys	Gly	Lys	Cys	Pro	Pro	His	Ser	Tyr	Thr		
		290				295						300					
CAT	GAG	GAA	GCT	TCA	ACC	TCT	TGT	GTC	TGT	GAA	AAG	GAT	TAT	TTC	AGG		960
His	Glu	Glu	Ala	Ser	Thr	Ser	Cys	Val	Cys	Glu	Lys	Asp	Tyr	Phe	Arg		
305					310					315					320		
AGA	GAG	TCT	GAT	CCA	CCC	ACA	ATG	GCA	TGC	ACA	AGA	CCC	CCC	TCT	GCT		1008
Arg	Glu	Ser	Asp	Pro	Pro	Thr	Met	Ala	Cys	Thr	Arg	Pro	Pro	Ser	Ala		
				325					330					335			
CCT	CGG	AAT	GCC	ATC	TCA	AAT	GTT	AAT	GAA	ACT	AGT	GTC	TTT	CTG	GAA		1056
Pro	Arg	Asn	Ala	Ile	Ser	Asn	Val	Asn	Glu	Thr	Ser	Val	Phe	Leu	Glu		
			340					345					350				
TGG	ATT	CCG	CCT	GCT	GAC	ACT	GGT	GGA	AGG	AAA	GAC	GTG	TCA	TAT	TAT		1104
Trp	Ile	Pro	Pro	Ala	Asp	Thr	Gly	Gly	Arg	Lys	Asp	Val	Ser	Tyr	Tyr		
		355					360					365					
ATT	GCA	TGC	AAG	AAG	TGC	AAC	TCC	CAT	GCA	GGT	GTG	TGT	GAG	GAG	TGT		1152
Ile	Ala	Cys	Lys	Lys	Cys	Asn	Ser	His	Ala	Gly	Val	Cys	Glu	Glu	Cys		
		370				375					380						
GGC	GGT	CAT	GTC	AGG	TAC	CTT	CCC	CGG	CAA	AGC	GGC	CTG	AAA	AAC	ACC		1200
Gly	Gly	His	Val	Arg	Tyr	Leu	Pro	Arg	Gln	Ser	Gly	Leu	Lys	Asn	Thr		
385					390					395					400		
TCT	GTC	ATG	ATG	GTG	GAT	CTA	CTC	GCT	CAC	ACA	AAC	TAT	ACC	TTT	GAG		1248
Ser	Val	Met	Met	Val	Asp	Leu	Leu	Ala	His	Thr	Asn	Tyr	Thr	Phe	Glu		
				405					410					415			

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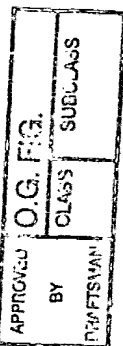


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## FIG. 2C

ATT GAG GCA GTG AAT GGA GTG TCC GAC TTG AGC CCA GGA GCC CGG CAG Ile Glu Ala Val Asn Gly Val Ser Asp Leu Ser Pro Gly Ala Arg Gln 420 425 430	1296
TAT GTG TCT GTA AAT GTA ACC ACA AAT CAA GCA GCT CCA TCT CCA GTC Tyr Val Ser Val Asn Val Thr Thr Asn Gln Ala Ala Pro Ser Pro Val 435 440 445	1344
ACC AAT GTG AAA AAA GGG AAA ATT GCA AAA AAC AGC ATC TCT TTG TCT Thr Asn Val Lys Lys Gly Lys Ile Ala Lys Asn Ser Ile Ser Leu Ser 450 455 460	1392
TGG CAA GAA CCA GAT CGT CCC AAT GGA ATC ATC CTA GAG TAT GAA ATC Trp Gln Glu Pro Asp Arg Pro Asn Gly Ile Ile Leu Glu Tyr Glu Ile 465 470 475 480	1440
AAG CAT TTT GAA AAG GAC CAA GAG ACC AGC TAC ACG ATT ATC AAA TCT Lys His Phe Glu Lys Asp Gln Glu Thr Ser Tyr Thr Ile Ile Lys Ser 485 490 495	1488
AAA GAG ACA ACT ATT ACT GCA GAG GGC TTG AAA CCA GCT TCA GTT TAT Lys Glu Thr Thr Ile Thr Ala Glu Gly Leu Lys Pro Ala Ser Val Tyr 500 505 510	1536
GTC TTC CAA ATT CGA GCA CGT ACA GCA GCA GGC TAT GGT GTC TTC AGT Val Phe Gln Ile Arg Ala Arg Thr Ala Ala Gly Tyr Gly Val Phe Ser 515 520 525	1584
CGA AGA TTT GAG TTT GAA ACC ACC CCA GTG TTT GCA GCA TCC AGC GAT Arg Arg Phe Glu Phe Glu Thr Thr Pro Val Phe Ala Ala Ser Ser Asp 530 535 540	1632
CAA AGC CAG ATT CCT GTA ATT GCT GTG TCT GTG ACA GTA GGA GTC ATT Gln Ser Gln Ile Pro Val Ile Ala Val Ser Val Thr Val Gly Val Ile 545 550 555 560	1680
TTG TTG GCA GTG GTT ATC GGC GTC CTC CTC AGT GGA AGG CGG TGT GGC Leu Leu Ala Val Val Ile Gly Val Leu Leu Ser Gly Arg Arg Cys Gly 565 570 575	1728
TAC AGC AAA GCA AAA CAA GAT CCA GAA GAG GAA AAG ATG CAT TTT CAT Tyr Ser Lys Ala Lys Gln Asp Pro Glu Glu Glu Lys Met His Phe His 580 585 590	1776
AAT GGG CAC ATT AAA CTG CCA GGA GTA AGA ACT TAC ATT GAT CCA CAT Asn Gly His Ile Lys Leu Pro Gly Val Arg Thr Tyr Ile Asp Pro His 595 600 605	1824
ACC TAT GAG GAT CCC AAT CAA GCT GTC CAC GAA TTT GCC AAG GAG ATA Thr Tyr Glu Asp Pro Asn Gln Ala Val His Glu Phe Ala Lys Glu Ile 610 615 620	1872







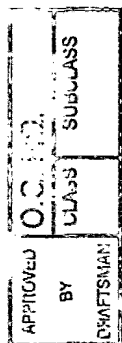
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# FIG. 2D

GAA GCA TCA TGT ATC ACC ATT GAG AGA GTT ATT GGA GCA GGT GAA TTT	1920
Glu Ala Ser Cys Ile Thr Ile Glu Arg Val Ile Gly Ala Gly Glu Phe	
625 630 635 640	
GGT GAA GTT TGT AGT GGA CGT TTG AAA CTA CCA GGA AAA AGA GAA TTA	1968
Gly Glu Val Cys Ser Gly Arg Leu Lys Leu Pro Gly Lys Arg Glu Leu	
645 650 655	
CCT GTG GCT ATC AAA ACC CTT AAA GTA GGC TAT ACT GAA AAG CAA CGC	2016
Pro Val Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr Glu Lys Gln Arg	
660 665 670	
AGA GAT TTC CTA GGT GAA GCA AGT ATC ATG GGA CAG TTT GAT CAT CCT	2064
Arg Asp Phe Leu Gly Glu Ala Ser Ile Met Gly Gln Phe Asp His Pro	
675 680 685	
AAC ATC ATC CAT TTA GAA GGT GTG GTG ACC AAA AGT AAA CCA GTG ATG	2112
Asn Ile Ile His Leu Glu Gly Val Val Thr Lys Ser Lys Pro Val Met	
690 695 700	
ATC GTG ACA GAG TAT ATG GAG AAT GGC TCT TTA GAT ACA TTT TTG AAG	2160
Ile Val Thr Glu Tyr Met Glu Asn Gly Ser Leu Asp Thr Phe Leu Lys	
705 710 715 720	
AAA AAC GAT GGG CAG TTC ACT GTG ATT CAG CTT GTT GGC ATG CTG AGA	2208
Lys Asn Asp Gly Gln Phe Thr Val Ile Gln Leu Val Gly Met Leu Arg	
725 730 735	
GGT ATC TCT GCA GGA ATG AAG TAC CTT TCT GAC ATG GGC TAT GTG CAT	2256
Gly Ile Ser Ala Gly Met Lys Tyr Leu Ser Asp Met Gly Tyr Val His	
740 745 750	
AGA GAT CTT GCT GCC AGA AAC ATC TTA ATC AAC AGT AAC CTT GTG TGC	2304
Arg Asp Leu Ala Ala Arg Asn Ile Leu Ile Asn Ser Asn Leu Val Cys	
755 760 765	
AAA GTG TCT GAC TTT GGA CTT TCC CGG GTA CTG GAA GAT GAT CCC GAG	2352
Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro Glu	
770 775 780	
GCA GCC TAC ACC ACA AGG GGA GGA AAA ATT CCA ATC AGA TGG ACT GCC	2400
Ala Ala Tyr Thr Thr Arg Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala	
785 790 795 800	
CCA GAA GCA ATA GCT TTC CGA AAG TTT ACT TCT GCC AGT GAT GTC TGG	2448
Pro Glu Ala Ile Ala Phe Arg Lys Phe Thr Ser Ala Ser Asp Val Trp	
805 810 815	
AGT TAT GGA ATA GTA ATG TGG GAA GTT GTG TCT TAT GGA GAG AGA CCC	2496
Ser Tyr Gly Ile Val Met Trp Glu Val Val Ser Tyr Gly Glu Arg Pro	
820 825 830	



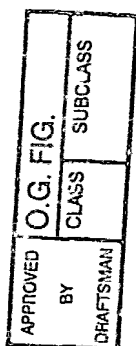


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## FIG. 2E

TAC TGG GAG ATG ACC AAT CAA GAT GTG ATT AAA GCG GTA GAG GAA GGC	
Tyr Trp Glu Met Thr Asn Gln Asp Val Ile Lys Ala Val Glu Glu Gly	
835	840 845
TAT CGT CTG CCA AGC CCC ATG GAT TGT CCT GCT GCT CTC TAT CAG TTA	2592
Tyr Arg Leu Pro Ser Pro Met Asp Cys Pro Ala Ala Leu Tyr Gln Leu	
850	855 860
ATG CTG GAT TGC TGG CAG AAA GAG CGA AAT AGC AGG CCC AAG TTT GAT	2640
Met Leu Asp Cys Trp Gln Lys Glu Arg Asn Ser Arg Pro Lys Phe Asp	
865	870 875 880
GAA ATA GTC AAC ATG TTG GAC AAG CTG ATA CGT AAC CCA AGT AGT CTG	2688
Glu Ile Val Asn Met Leu Asp Lys Leu Ile Arg Asn Pro Ser Ser Leu	
885	890 895
AAG ACG CTG GTT AAT GCA TCC TGC AGA GTA TCT AAT TTA TTG GCA GAA	2736
Lys Thr Leu Val Asn Ala Ser Cys Arg Val Ser Asn Leu Leu Ala Glu	
900	905 910
CAT AGC CCA CTA GGA TCT GGG GCC TAC AGA TCA GTA GGT GAA TGG CTA	2784
His Ser Pro Leu Gly Ser Gly Ala Tyr Arg Ser Val Gly Glu Trp Leu	
915	920 925
GAG GCA ATC AAG ATG GGC CGG TAT ACA GAG ATT TTC ATG GAA AAT GGA	2832
Glu Ala Ile Lys Met Gly Arg Tyr Thr Glu Ile Phe Met Glu Asn Gly	
930	935 940
TAC AGT TCA ATG GAC GCT GTG GCT CAG GTG ACC TTG GAG GAT TTG AGA	2880
Tyr Ser Ser Met Asp Ala Val Ala Gln Val Thr Leu Glu Asp Leu Arg	
945	950 955 960
CGG CTT GGA GTG ACT CTT GTC GGT CAC CAG AAG AAG ATC ATG AAC AGC	2928
Arg Leu Gly Val Thr Leu Val Gly His Gln Lys Lys Ile Met Asn Ser	
965	970 975
CTT CAA GAA ATG AAG GTG CAG CTG GTA AAC GGA ATG GTG CCA TTG TAACTTCATG	
2983	
Leu Gln Glu Met Lys Val Gln Leu Val Asn Gly Met Val Pro Leu	
980	985 990
TAAATGTCGC TTCTTCAAGT GAATGATTCT GCACTTTGTA AACAGCACTG AGATTTATTT	3043
TAACAAAAAA AGGGGGAAAA GGGAAAACAG TGATTTCTAA ACCTTAGAAA ACATTTGCCT	3103
CAGCCACAGA ATTTGTAATC ATGGTTTTAC TGAAGTATCC AGTTCTTAGT CCTTAGTCT	3162





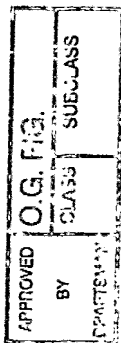
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# FIG. 3A

AAGCGGCAGG AGCAGCGTTG GCACCGGCGA ACC ATG GCT GGG ATT TTC TAT TTC	54
Met Ala Gly Ile Phe Tyr Phe	
1 5	
GCC CTA TTT TCG TGT CTC TTC GGG ATT TGC GAC GCT GTC ACA GGT TCC	102
Ala Leu Phe Ser Cys Leu Phe Gly Ile Cys Asp Ala Val Thr Gly Ser	
10 15 20	
AGG GTA TAC CCC GCG AAT GAA GTT ACC TTA TTG GAT TCC AGA TCT GTT	150
Arg Val Tyr Pro Ala Asn Glu Val Thr Leu Leu Asp Ser Arg Ser Val	
25 30 35	
CAG GGA GAA CTT GGG TGG ATA GCA AGC CCT CTG GAA GGA GGG TGG GAG	198
Gln Gly Glu Leu Gly Trp Ile Ala Ser Pro Leu Glu Gly Gly Trp Glu	
40 45 50 55	
GAA GTG AGT ATC ATG GAT GAA AAA AAT ACA CCA ATC CGA ACC TAC CAA	246
Glu Val Ser Ile Met Asp Glu Lys Asn Thr Pro Ile Arg Thr Tyr Gln	
60 65 70	
GTG TGC AAT GTG ATG GAA CCC AGC CAG AAT AAC TGG CTA CGA ACT GAT	294
Val Cys Asn Val Met Glu Pro Ser Gln Asn Asn Trp Leu Arg Thr Asp	
75 80 85	
TGG ATC ACC CGA GAA GGG GCT CAG AGG GTG TAT ATT GAG ATT AAA TTC	342
Trp Ile Thr Arg Glu Gly Ala Gln Arg Val Tyr Ile Glu Ile Lys Phe	
90 95 100	
ACC TTG AGG GAC TGC AAT AGT CTT CCG GGC GTC ATG GGG ACT TGC AAG	390
Thr Leu Arg Asp Cys Asn Ser Leu Pro Gly Val Met Gly Thr Cys Lys	
105 110 115	
GAG ACG TTT AAC CTG TAC TAC TAT GAA TCA GAC AAC GAC AAA GAG CGT	438
Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu Ser Asp Asn Asp Lys Glu Arg	
120 125 130 135	
TTC ATC AGA GAG AAC CAG TTT GTC AAA ATT GAC ACC ATT GCT GCT GAT	486
Phe Ile Arg Glu Asn Gln Phe Val Lys Ile Asp Thr Ile Ala Ala Asp	
140 145 150	
GAG AGC TTC ACC CAA GTG GAC ATT GGT GAC AGA ATC ATG AAG CTG AAC	534
Glu Ser Phe Thr Gln Val Asp Ile Gly Asp Arg Ile Met Lys Leu Asn	
155 160 165	
ACC GAG ATC CGG GAT GTA GGG CCA TTA AGC AAA AAG GGG TTT TAC CTG	582
Thr Glu Ile Arg Asp Val Gly Pro Leu Ser Lys Lys Gly Phe Tyr Leu	
170 175 180	

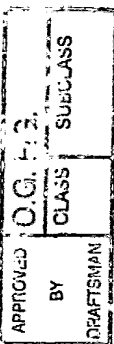




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# FIG. 3B

GCT	TTT	CAG	GAT	GTG	GGG	GCC	TGC	ATC	GCC	CTG	GTA	TCA	GTC	CGT	GTG	630
Ala	Phe	Gln	Asp	Val	Gly	Ala	Cys	Ile	Ala	Leu	Val	Ser	Val	Arg	Val	
185						190					195					
TTC	TAT	AAA	AAG	TGT	CCA	CTC	ACA	GTC	CGC	AAT	CTG	GCC	CAG	TTT	CCT	678
Phe	Tyr	Lys	Lys	Cys	Pro	Leu	Thr	Val	Arg	Asn	Leu	Ala	Gln	Phe	Pro	
200						205				210					215	
GAC	ACC	ATC	ACA	GGG	GCT	GAT	ACG	TCT	TCC	CTG	GTG	GAA	GTT	CGA	GGC	726
Asp	Thr	Ile	Thr	Gly	Ala	Asp	Thr	Ser	Ser	Leu	Val	Glu	Val	Arg	Gly	
				220					225					230		
TCC	TGT	GTC	AAC	AAC	TCA	GAA	GAG	AAA	GAT	GTG	CCA	AAA	ATG	TAC	TGT	774
Ser	Cys	Val	Asn	Asn	Ser	Glu	Glu	Lys	Asp	Val	Pro	Lys	Met	Tyr	Cys	
			235					240					245			
GGG	GCA	GAT	GGT	GAA	TGG	CTG	GTA	CCC	ATT	GGC	AAC	TGC	CTA	TGC	AAC	822
Gly	Ala	Asp	Gly	Glu	Trp	Leu	Val	Pro	Ile	Gly	Asn	Cys	Leu	Cys	Asn	
		250					255					260				
GCT	GGG	CAT	GAG	GAG	CGG	AGC	GGA	GAA	TGC	CAA	GCT	TGC	AAA	ATT	GGA	870
Ala	Gly	His	Glu	Glu	Arg	Ser	Gly	Glu	Cys	Gln	Ala	Cys	Lys	Ile	Gly	
	265					270					275					
TAT	TAC	AAG	GCT	CTC	TCC	ACG	GAT	GCC	ACC	TGT	GCC	AAG	TGC	CCA	CCC	918
Tyr	Tyr	Lys	Ala	Leu	Ser	Thr	Asp	Ala	Thr	Cys	Ala	Lys	Cys	Pro	Pro	
280						285				290					295	
CAC	AGC	TAC	TCT	GTC	TGG	GAA	GGA	GCC	ACC	TCG	TGC	ACC	TGT	GAC	CGA	966
His	Ser	Tyr	Ser	Val	Trp	Glu	Gly	Ala	Thr	Ser	Cys	Thr	Cys	Asp	Arg	
				300					305					310		
GGC	TTT	TTC	AGA	GCT	GAC	AAC	GAT	GCT	GCC	TCT	ATG	CCC	TGC	ACC	CGT	1014
Gly	Phe	Phe	Arg	Ala	Asp	Asn	Asp	Ala	Ala	Ser	Met	Pro	Cys	Thr	Arg	
			315					320					325			
CCA	CCA	TCT	GCT	CCC	CTG	AAC	TTG	ATT	TCA	AAT	GTC	AAC	GAG	ACA	TCT	1062
Pro	Pro	Ser	Ala	Pro	Leu	Asn	Leu	Ile	Ser	Asn	Val	Asn	Glu	Thr	Ser	
		330					335					340				
GTG	AAC	TTG	GAA	TGG	AGT	AGC	CCT	CAG	AAT	ACA	GGT	GGC	CGC	CAG	GAC	1110
Val	Asn	Leu	Glu	Trp	Ser	Ser	Pro	Gln	Asn	Thr	Gly	Gly	Arg	Gln	Asp	
	345					350					355					
ATT	TCC	TAT	AAT	GTG	GTA	TGC	AAG	AAA	TGT	GGA	GCT	GGT	GAC	CCC	AGC	1158
Ile	Ser	Tyr	Asn	Val	Val	Cys	Lys	Lys	Cys	Gly	Ala	Gly	Asp	Pro	Ser	
360					365					370					375	
AAG	TGC	CGA	CCC	TGT	GGA	AGT	GGG	GTC	CAC	TAC	ACC	CCA	CAG	CAG	AAT	1206
Lys	Cys	Arg	Pro	Cys	Gly	Ser	Gly	Val	His	Tyr	Thr	Pro	Gln	Gln	Asn	
				380					385					390		





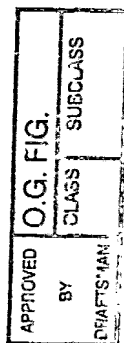
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FIG. 3C

GGC TTG AAG ACC ACC AAA GTC TCC ATC ACT GAC CTC CTA GCT CAT ACC	1254
Gly Leu Lys Thr Thr Lys Val Ser Ile Thr Asp Leu Leu Ala His Thr	
395 400 405	
AAT TAC ACC TTT GAA ATC TGG GCT GTG AAT GGA GTG TCC AAA TAT AAC	1302
Asn Tyr Thr Phe Glu Ile Trp Ala Val Asn Gly Val Ser Lys Tyr Asn	
410 415 420	
CCT AAC CCA GAC CAA TCA GTT TCT GTC ACT GTG ACC ACC AAC CAA GCA	1350
Pro Asn Pro Asp Gln Ser Val Ser Val Thr Val Thr Thr Asn Gln Ala	
425 430 435	
GCA CCA TCA TCC ATT GCT TTG GTC CAG GCT AAA GAA GTC ACA AGA TAC	1398
Ala Pro Ser Ser Ile Ala Leu Val Gln Ala Lys Glu Val Thr Arg Tyr	
440 445 450 455	
AGT GTG GCA CTG GCT TGG CTG GAA CCA GAT CGG CCC AAT GGG GTA ATC	1446
Ser Val Ala Leu Ala Trp Leu Glu Pro Asp Arg Pro Asn Gly Val Ile	
460 465 470	
CTG GAA TAT GAA GTC AAG TAT TAT GAG AAG GAT CAG AAT GAG CGA AGC	1494
Leu Glu Tyr Glu Val Lys Tyr Tyr Glu Lys Asp Gln Asn Glu Arg Ser	
475 480 485	
TAT CGT ATA GTT CGG ACA GCT GCC AGG AAC ACA GAT ATC AAA GGC CTG	1542
Tyr Arg Ile Val Arg Thr Ala Ala Arg Asn Thr Asp Ile Lys Gly Leu	
490 495 500	
AAC CCT CTC ACT TCC TAT GTT TTC CAC GTG CGA GCC AGG ACA GCA GCT	1590
Asn Pro Leu Thr Ser Tyr Val Phe His Val Arg Ala Arg Thr Ala Ala	
505 510 515	
GGC TAT GGA GAC TTC AGT GAG CCC TTG GAG GTT ACA ACC AAC ACA GTG	1638
Gly Tyr Gly Asp Phe Ser Glu Pro Leu Glu Val Thr Thr Asn Thr Val	
520 525 530 535	
CCT TCC CGG ATC ATT GGA GAT GGG GCT AAC TCC ACA GTC CTT CTG GTC	1686
Pro Ser Arg Ile Ile Gly Asp Gly Ala Asn Ser Thr Val Leu Leu Val	
540 545 550	
TCT GTC TCG GGC AGT GTG GTG CTG GTG GTA ATT CTC ATT GCA GCT TTT	1734
Ser Val Ser Gly Ser Val Val Leu Val Val Ile Leu Ile Ala Ala Phe	
555 560 565	
GTC ATC AGC CGG AGA CGG AGT AAA TAC AGT AAA GCC AAA CAA GAA GCG	1782
Val Ile Ser Arg Arg Arg Ser Lys Tyr Ser Lys Ala Lys Gln Glu Ala	
570 575 580	
GAT GAA GAG AAA CAT TTG AAT CAA GGT GTA AGA ACA TAT GTG GAC CCC	1830
Asp Glu Glu Lys His Leu Asn Gln Gly Val Arg Thr Tyr Val Asp Pro	
585 590 595	





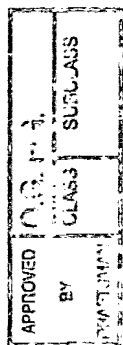
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FIG. 3D

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TTT	ACG	TAC	GAA	GAT	CCC	AAC	CAA	GCA	GTG	CGA	GAG	TTT	GCC	AAA	GAA	1878
Phe	Thr	Tyr	Glu	Asp	Pro	Asn	Gln	Ala	Val	Arg	Glu	Phe	Ala	Lys	Glu	
600					605				610						615	
ATT	GAC	GCA	TCC	TGC	ATT	AAG	ATT	GAA	AAA	GTT	ATA	GGA	GTT	GGT	GAA	1926
Ile	Asp	Ala	Ser	Cys	Ile	Lys	Ile	Glu	Lys	Val	Ile	Gly	Val	Gly	Glu	
				620					625						630	
TTT	GGT	GAG	GTA	TGC	AGT	GGG	CGT	CTC	AAA	GTG	CCT	GGC	AAG	AGA	GAG	1974
Phe	Gly	Glu	Val	Cys	Ser	Gly	Arg	Leu	Lys	Val	Pro	Gly	Lys	Arg	Glu	
			635					640						645		
ATC	TGT	GTG	GCT	ATC	AAG	ACT	CTG	AAA	GCT	GGT	TAT	ACA	GAC	AAA	CAG	2022
Ile	Cys	Val	Ala	Ile	Lys	Thr	Leu	Lys	Ala	Gly	Tyr	Thr	Asp	Lys	Gln	
		650					655						660			
AGG	AGA	GAC	TTC	CTG	AGT	GAG	GCC	AGC	ATC	ATG	GGA	CAG	TTT	GAC	CAT	2070
Arg	Arg	Asp	Phe	Leu	Ser	Glu	Ala	Ser	Ile	Met	Gly	Gln	Phe	Asp	His	
		665				670						675				
CCG	AAC	ATC	ATT	CAC	TTG	GAA	GGC	GTG	GTC	ACT	AAA	TGT	AAA	CCA	GTA	2118
Pro	Asn	Ile	Ile	His	Leu	Glu	Gly	Val	Val	Thr	Lys	Cys	Lys	Pro	Val	
					685					690					695	
ATG	ATC	ATA	ACA	GAG	TAC	ATG	GAG	AAT	GGC	TCC	TTG	GAT	GCA	TTC	CTC	2166
Met	Ile	Ile	Thr	Glu	Tyr	Met	Glu	Asn	Gly	Ser	Leu	Asp	Ala	Phe	Leu	
				700					705					710		
AGG	AAA	AAT	GAT	GGC	AGA	TTT	ACA	GTC	ATT	CAG	CTG	GTG	GGC	ATG	CTT	2214
Arg	Lys	Asn	Asp	Gly	Arg	Phe	Thr	Val	Ile	Gln	Leu	Val	Gly	Met	Leu	
			715					720					725			
CGT	GGC	ATT	GGG	TCT	GGG	ATG	AAG	TAT	TTA	TCT	GAT	ATG	AGC	TAT	GTG	2262
Arg	Gly	Ile	Gly	Ser	Gly	Met	Lys	Tyr	Leu	Ser	Asp	Met	Ser	Tyr	Val	
		730					735					740				
CAT	CGT	GAT	CTG	GCC	GCA	CGG	AAC	ATC	CTG	GTG	AAC	AGC	AAC	TTG	GTC	2310
His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Val	Asn	Ser	Asn	Leu	Val	
		745				750					755					
TGC	AAA	GTG	TCT	GAT	TTT	GGC	ATG	TCC	CGA	GTG	CTT	GAG	GAT	GAT	CCG	2358
Cys	Lys	Val	Ser	Asp	Phe	Gly	Met	Ser	Arg	Val	Leu	Glu	Asp	Asp	Pro	
		760			765					770					775	
GAA	GCA	GCT	TAC	ACC	ACC	AGG	GGT	GGC	AAG	ATT	CCT	ATC	CGG	TGG	ACT	2406
Glu	Ala	Ala	Tyr	Thr	Thr	Arg	Gly	Gly	Lys	Ile	Pro	Ile	Arg	Trp	Thr	
				780					785					790		
GCG	CCA	GAA	GCA	ATT	GCC	TAT	CGT	AAA	TTC	ACA	TCA	GCA	AGT	GAT	GTA	2454
Ala	Pro	Glu	Ala	Ile	Ala	Tyr	Arg	Lys	Phe	Thr	Ser	Ala	Ser	Asp	Val	
			795					800					805			



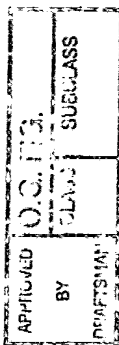


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# FIG. 3E

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TGG AGC TAT GGA ATC GTT ATG TGG GAA GTG ATG TCG TAC GGG GAG AGG	
Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr Gly Glu Arg	
810 815 820	
CCC TAT TGG GAT ATG TCC AAT CAA GAT GTG ATT AAA GCC ATT GAG GAA	2550
Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala Ile Glu Glu	
825 830 835	
GGC TAT CGG TTA CCC CCT CCA ATG GAC TGC CCC ATT GCG CTC CAC CAG	2598
Gly Tyr Arg Leu Pro Pro Pro Met Asp Cys Pro Ile Ala Leu His Gln	
840 845 850 855	
CTG ATG CTA GAC TGC TGG CAG AAG GAG AGG AGC GAC AGG CCT AAA TTT	2646
Leu Met Leu Asp Cys Trp Gln Lys Glu Arg Ser Asp Arg Pro Lys Phe	
860 865 870	
GGG CAG ATT GTC AAC ATG TTG GAC AAA CTC ATC CGC AAC CCC AAC AGC	2694
Gly Gln Ile Val Asn Met Leu Asp Lys Leu Ile Arg Asn Pro Asn Ser	
875 880 885	
TTG AAG AGG ACA GGG ACG GAG AGC TCC AGA CCT AAC ACT GCC TTG TTG	2742
Leu Lys Arg Thr Gly Thr Glu Ser Ser Arg Pro Asn Thr Ala Leu Leu	
890 895 900	
GAT CCA AGC TCC CCT GAA TTC TCT GCT GTG GTA TCA GTG GGC GAT TGG	2790
Asp Pro Ser Ser Pro Glu Phe Ser Ala Val Val Ser Val Gly Asp Trp	
905 910 915	
CTC CAG GCC ATT AAA ATG GAC CGG TAT AAG GAT AAC TTC ACA GCT GCT	2838
Leu Gln Ala Ile Lys Met Asp Arg Tyr Lys Asp Asn Phe Thr Ala Ala	
920 925 930 935	
GGT TAT ACC ACA CTA GAG GCT GTG GTG CAC GTG AAC CAG GAG GAC CTG	2886
Gly Tyr Thr Thr Leu Glu Ala Val Val His Val Asn Gln Glu Asp Leu	
940 945 950	
GCA AGA ATT GGT ATC ACA GCC ATC ACG CAC CAG AAT AAG ATT TTG AGC	2934
Ala Arg Ile Gly Ile Thr Ala Ile Thr His Gln Asn Lys Ile Leu Ser	
955 960 965	
AGT GTC CAG GCA ATG CGA ACC CAA ATG CAG CAG ATG CAC GGC AGA ATG	2982
Ser Val Gln Ala Met Arg Thr Gln Met Gln Gln Met His Gly Arg Met	
970 975 980	
GTT CCC GTC TGAGCCAGTA CTGAATAAAC TCAAACTCT TGAAATTAGT	3031
Val Pro Val	
985	
TTACCTCATC CATGCACTTT AATTGAAGAA CTGCACTTTT TTTACTTCGT CTTCGCCCTC	3091
TGAAATTAAA GAAATGAAAA AAAAA	3116





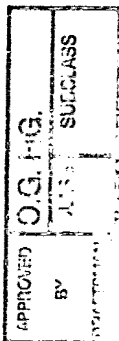
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## FIG. 4A

CGGTGCGAGC GAACAGGAGT GGGGGGGAAA TTAAAAAAG CTAAACGTGG AGCAGCCGAT	60
CGGGGACCGA GAAGGGGAAT CGATGCAAGG AGCACACTAA AACAAAAGCT ACTTCGGAAC	120
AAACAGCATT TAAAAATCCA CGACTCAAGA TAACTGAAAC CTAAAATAAA ACCTGCTCAT	180
GCACC ATG GTT TTT CAA ACT CGG TAC CCT TCA TGG ATT ATT TTA TGC Met Val Phe Gln Thr Arg Tyr Pro Ser Trp Ile Ile Leu Cys	227
1 5 10	
TAC ATC TGG CTG CTC CGC TTT GCA CAC ACA GGG GAG GCG CAG GCT GCG Tyr Ile Trp Leu Leu Arg Phe Ala His Thr Gly Glu Ala Gln Ala Ala	275
15 20 25 30	
AAG GAA GTA CTA CTG CTG GAT TCT AAA GCA CAA CAA ACA GAG TTG GAG Lys Glu Val Leu Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu	323
35 40 45	
TGG ATT TCC TCT CCA CCC AAT GGG TGG GAA GAA ATT AGT GGT TTG GAT Trp Ile Ser Ser Pro Pro Asn Gly Trp Glu Glu Ile Ser Gly Leu Asp	371
50 55 60	
GAG AAC TAT ACC CCG ATA CGA ACA TAC CAG GTG TGC CAA GTC ATG GAG Glu Asn Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu	419
65 70 75	
CCC AAC CAA AAC AAC TGG CTG CGG ACT AAC TGG ATT TCC AAA GGC AAT Pro Asn Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn	467
80 85 90	
GCA CAA AGG ATT TTT GTA GAA TTG AAA TTC ACC CTG AGG GAT TGT AAC Ala Gln Arg Ile Phe Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn	515
95 100 105 110	
AGT CTT CCT GGA GTA CTG GGA ACT TGC AAG GAA ACA TTT AAT TTG TAC Ser Leu Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr	563
115 120 125	
TAT TAT GAA ACA GAC TAT GAC ACT GGC AGG AAT ATA AGA GAA AAC CTC Tyr Tyr Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu	611
130 135 140	
TAT GTA AAA ATA GAC ACC ATT GCT GCA GAT GAA AGT TTT ACC CAA GGT Tyr Val Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly	659
145 150 155	
GAC CTT GGT GAA AGA AAG ATG AAG CTT AAC ACT GAG GTG AGA GAG ATT Asp Leu Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile	707
160 165 170	







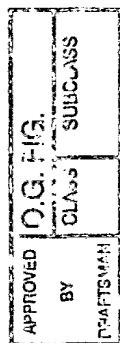
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# FIG. 4B

GGA CCT TTG TCC AAA AAG GGA TTC TAT CTT GCC TTT CAG GAT GTA GGG	755
Gly Pro Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly	
175 180 185 190	
GCT TGC ATA GCT TTG GTT TCT GTC AAA GTG TAC TAC AAG AAG TGC TGG	803
Ala Cys Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp	
195 200 205	
TCC ATT ATT GAG AAC TTA GCT ATC TTT CCA GAT ACA GTG ACT GGT TCA	851
Ser Ile Ile Glu Asn Leu Ala Ile Phe Pro Asp Thr Val Thr Gly Ser	
210 215 220	
GAA TTT TCC TCT TTA GTC GAG GTT CGA GGG ACA TGT GTC AGC AGT GCA	899
Glu Phe Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala	
225 230 235	
GAG GAA GAA GCG GAA AAC GCC CCC AGG ATG CAC TGC AGT GCA GAA GGA	947
Glu Glu Glu Ala Glu Asn Ala Pro Arg Met His Cys Ser Ala Glu Gly	
240 245 250	
GAA TGG TTA GTG CCC ATT GGA AAA TGT ATC TGC AAA GCA GGC TAC CAG	995
Glu Trp Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln	
255 260 265 270	
CAA AAA GGA GAC ACT TGT GAA CCC TGT GGC CGT GGG TTC TAC AAG TCT	1043
Gln Lys Gly Asp Thr Cys Glu Pro Cys Gly Arg Gly Phe Tyr Lys Ser	
275 280 285	
TCC TCT CAA GAT CTT CAG TGC TCT CGT TGT CCA ACT CAC AGT TTT TCT	1091
Ser Ser Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser	
290 295 300	
GAT AAA GAA GGC TCC TCC AGA TGT GAA TGT GAA GAT GGG TAT TAC AGG	1139
Asp Lys Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg	
305 310 315	
GCT CCA TCT GAC CCA CCA TAC GTT GCA TGC ACA AGG CCT CCA TCT GCA	1187
Ala Pro Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala	
320 325 330	
CCA CAG AAC CTC ATT TTC AAC ATC AAC CAA ACC ACA GTA AGT TTG GAA	1235
Pro Gln Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu	
335 340 345 350	
TGG AGT CCT CCT GCA GAC AAT GGG GGA AGA AAC GAT GTG ACC TAC AGA	1283
Trp Ser Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg	
355 360 365	
ATA TTG TGT AAG CGG TGC AGT TGG GAG CAG GGC GAA TGT GTT CCC TGT	1331
Ile Leu Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys	
370 375 380	



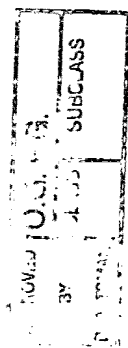


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# FIG. 4C

GGG AGT AAC ATT GGA TAC ATG CCC CAG CAG ACT GGA TTA GAG GAT AAC	1379
Gly Ser Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn	
385 390 395	
TAT GTC ACT GTC ATG GAC CTG CTA GCC CAC GCT AAT TAT ACT TTT GAA	1427
Tyr Val Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu	
400 405 410	
GTT GAA GCT GTA AAT GGA GTT TCT GAC TTA AGC CGA TCC CAG AGG CTC	1475
Val Glu Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu	
415 420 425 430	
TTT GCT GCT GTC AGT ATC ACC ACT GGT CAA GCA GCT CCC TCG CAA GTG	1523
Phe Ala Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val	
435 440 445	
AGC GGA GTA ATG AAG GAG AGA GTA CTG CAG CGG AGT GTC GAG CTT TCC	1571
Ser Gly Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Glu Leu Ser	
450 455 460	
TGG CAG GAA CCA GAG CAT CCC AAT GGA GTC ATC ACA GAA TAT GAA ATC	1619
Trp Gln Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile	
465 470 475	
AAG TAT TAC GAG AAA GAT CAA AGG GAA CGG ACC TAC TCA ACA GTA AAA	1667
Lys Tyr Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Val Lys	
480 485 490	
ACC AAG TCT ACT TCA GCC TCC ATT AAT AAT CTG AAA CCA GGA ACA GTG	1715
Thr Lys Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val	
495 500 505 510	
TAT GTT TTC CAG ATT CGG GCT TTT ACT GCT GCT GGT TAT GGA AAT TAC	1763
Tyr Val Phe Gln Ile Arg Ala Phe Thr Ala Ala Gly Tyr Gly Asn Tyr	
515 520 525	
AGT CCC AGA CTT GAT GTT GCT ACA CTA GAG GAA GCT ACA GGT AAA ATG	1811
Ser Pro Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Thr Gly Lys Met	
530 535 540	
TTT GAA GCT ACA GCT GTC TCC AGT GAA CAG AAT CCT GTT ATT ATC ATT	1859
Phe Glu Ala Thr Ala Val Ser Ser Glu Gln Asn Pro Val Ile Ile Ile	
545 550 555	
GCT GTG GTT GCT GTA GCT GGG ACC ATC ATT TTG GTG TTC ATG GTC TTT	1907
Ala Val Val Ala Val Ala Gly Thr Ile Ile Leu Val Phe Met Val Phe	
560 565 570	
GGC TTC ATC ATT GGG AGA AGG CAC TGT GGT TAT AGC AAA GCT GAC CAA	1955
Gly Phe Ile Ile Gly Arg Arg His Cys Gly Tyr Ser Lys Ala Asp Gln	
575 580 585 590	





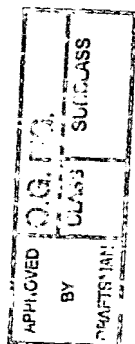
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# FIG. 4D

GAA GGC GAT GAA GAG CTT TAC TTT CAT TTT AAA TTT CCA GGC ACC AAA Glu Gly Asp Glu Glu Leu Tyr Phe His Phe Lys Phe Pro Gly Thr Lys 595 600 605	2003
ACC TAC ATT GAC CCT GAA ACC TAT GAG GAC CCA AAT AGA GCT GTC CAT Thr Tyr Ile Asp Pro Glu Thr Tyr Glu Asp Pro Asn Arg Ala Val His 610 615 620	2051
CAA TTC GCC AAG GAG CTA GAT GCC TCC TGT ATT AAA ATT GAG CGT GTG Gln Phe Ala Lys Glu Leu Asp Ala Ser Cys Ile Lys Ile Glu Arg Val 625 630 635	2099
ATT GGT GCA GGA GAA TTC GGT GAA GTC TGC AGT GGC CGT TTG AAA CTT Ile Gly Ala Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Leu 640 645 650	2147
CCA GGG AAA AGA GAT GTT GCA GTA GCC ATA AAA ACC CTG AAA GTT GGT Pro Gly Lys Arg Asp Val Ala Val Ala Ile Lys Thr Leu Lys Val Gly 655 660 665 670	2195
TAC ACA GAA AAA CAA AGG AGA GAC TTT TTG TGT GAA GCA AGC ATC ATG Tyr Thr Glu Lys Gln Arg Arg Asp Phe Leu Cys Glu Ala Ser Ile Met 675 680 685	2243
GGG CAG TTT GAC CAC CCA AAT GTT GTC CAT TTG GAA GGG GTT GTT ACA Gly Gln Phe Asp His Pro Asn Val Val His Leu Glu Gly Val Val Thr 690 695 700	2291
AGA GGG AAA CCA GTC ATG ATA GTA ATA GAG TTC ATG GAA AAT GGA GCC Arg Gly Lys Pro Val Met Ile Val Ile Glu Phe Met Glu Asn Gly Ala 705 710 715	2339
CTA GAT GCA TTT CTC AGG AAA CAT GAT GGG CAA TTT ACA GTC ATT CAG Leu Asp Ala Phe Leu Arg Lys His Asp Gly Gln Phe Thr Val Ile Gln 720 725 730	2387
TTA GTA GGA ATG CTG AGA GGA ATT GCT GCT GGA ATG AGA TAT TTG GCT Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Arg Tyr Leu Ala 735 740 745 750	2435
GAT ATG GGA TAT GTT CAC AGG GAC CTT GCA GCT CGC AAT ATT CTT GTC Asp Met Gly Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val 755 760 765	2483
AAC AGC AAT CTC GTT TGT AAA GTG TCA GAT TTT GGC CTG TCC CGA GTT Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val 770 775 780	2531
ATA GAG GAT GAT CCA GAA GCT GTC TAT ACA ACT ACT GGT GGA AAA ATT Ile Glu Asp Asp Pro Glu Ala Val Tyr Thr Thr Thr Gly Gly Lys Ile 785 790 795	2579





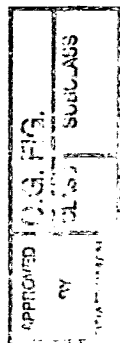
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FIG. 4E

CCA GTA AGG TGG ACA GCA CCC GAA GCC ATC CAG TAC CGG AAA TTC ACA	2627
Pro Val Arg Trp Thr Ala Pro Glu Ala Ile Gln Tyr Arg Lys Phe Thr	
800 805 810	
TCA GCC AGT GAT GTA TGG AGC TAT GGA ATA GTC ATG TGG GAA GTT ATG	2675
Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met	
815 820 825 830	
TCT TAT GGA GAA AGA CCT TAT TGG GAC ATG TCA AAT CAA GAT GTT ATA	2723
Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile	
835 840 845	
AAA GCA ATA GAA GAA GGT TAT CGT TTA CCA GCA CCC ATG GAC TGC CCA	2771
Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Ala Pro Met Asp Cys Pro	
850 855 860	
GCT GGC CTT CAC CAG CTA ATG TTG GAT TGT TGG CAA AAG GAG CGT GCT	2819
Ala Gly Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu Arg Ala	
865 870 875	
GAA AGG CCA AAA TTT GAA CAG ATA GTT GGA ATT CTA GAC AAA ATG ATT	2867
Glu Arg Pro Lys Phe Glu Gln Ile Val Gly Ile Leu Asp Lys Met Ile	
880 885 890	
CGA AAC CCA AAT AGT CTG AAA ACT CCC CTG GGA ACT TGT AGT AGG CCA	2915
Arg Asn Pro Asn Ser Leu Lys Thr Pro Leu Gly Thr Cys Ser Arg Pro	
895 900 905 910	
ATA AGC CCT CTT CTG GAT CAA AAC ACT CCT GAT TTC ACT ACC TTT TGT	2963
Ile Ser Pro Leu Leu Asp Gln Asn Thr Pro Asp Phe Thr Thr Phe Cys	
915 920 925	
TCA GTT GGA GAA TGG CTA CAA GCT ATT AAG ATG GAA AGA TAT AAA GAT	3011
Ser Val Gly Glu Trp Leu Gln Ala Ile Lys Met Glu Arg Tyr Lys Asp	
930 935 940	
AAT TTC ACG GCA GCT GGC TAC AAT TCC CTT GAA TCA GTA GCC AGG ATG	3059
Asn Phe Thr Ala Ala Gly Tyr Asn Ser Leu Glu Ser Val Ala Arg Met	
945 950 955	
ACT ATT GAG GAT GTG ATG AGT TTA GGG ATC ACA CTG GTT GGT CAT CAA	3107
Thr Ile Glu Asp Val Met Ser Leu Gly Ile Thr Leu Val Gly His Gln	
960 965 970	
AAG AAA ATC ATG AGC AGC ATT CAG ACT ATG AGA GCA CAA ATG CTA CAT	3155
Lys Lys Ile Met Ser Ser Ile Gln Thr Met Arg Ala Gln Met Leu His	
975 980 985 990	
TTA CAT GGA ACT GGC ATT CAA GTG TGATATGCAT TTCTCCCTTT TAAGGGAGAT	3209
Leu His Gly Thr Gly Ile Gln Val	
995	





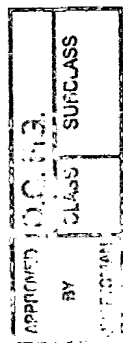
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# FIG. 4F

TACAGACTGC	AAGAGAACAG	TACTGGCCTT	CAGTATATGC	ATAGAATGCT	GCTAGAAGAC	3269
AAGTGATGTC	CTGGGTCCCT	CCAACAGTGA	AGAGAAGATT	TAAGAAGCAC	CTATAGACTT	3329
GAACTCCTAA	GTGCCACCAG	AATATATAAA	AAGGGAATTT	AGGATCCACC	ATCGGTGGCC	3389
AGGAAAATAG	CAGTGACAAT	AAACAAAGTA	CTACCTGAAA	AACATCCAAA	CACCTTGAGC	3449
TCTCTAACCT	CCTTTTTGTC	TTATAGACTT	TTTAAAATGT	ACATAAAGAA	TTTAAGAAAG	3509
AATATATTTG	TCAAATAAAA	TCATGATCTT	ATTGTTAAAA	TTAATGAAAT	ATTTTCCTTA	3569
AATATGTGAT	TTCAGACTAT	TCCTTTTTTAA	AATCATTGTG	GTTTATTCTT	CATAAGGACT	3629
TTGTTTTAGA	AAGCTGTTTA	TAGCTTTGGA	CCTTTTTAGT	GTTAAATCTG	TAACATTACT	3689
ACACTGGGTA	CCTTTGAAAG	AATCTCAAAT	TTCAAAAGAA	ATAGCATGAT	TGAAGATACA	3749
TCTCTGTTAG	AACATTGGTA	TCCTTTTTTGT	GCCATTTTAT	TCTGTTTAAT	CAGTGCTGTT	3809
TTGATATTGT	TTGCTAATTG	GCAGGTAGTC	AAGAAAATGC	AAGTTGCCAA	GAGCTCTGAT	3869
ATTTTTTAAA	AAGAATTTTT	TTGTAAAGAT	CAGACAACAC	ACTATCTTTT	CAATGAAAAA	3929
AGCAATAATG	ATCCATACAT	ACTATAAGGC	ACTTTTAACA	GATTGTTTAT	AGAGTGATTT	3989
TACTAGAAAG	AATTTAATAA	ACTCGAAGTT	TAGGTTTATG	AGTATATAAA	CAAATGAGGC	4049
ACTTCATCTG	AAGAATGTTG	GTGAAGGCAA	GTCTCTGAAA	GCAGAACTAT	CCAGTGTTAT	4109
CTAAAAATTA	ATCTGAGCAC	ATCAAGATTT	TTTCATTCTC	GTGACATTAG	GAAATTTAGG	4169
ATAAATAGTT	GACATATATT	TTATATCCTC	TTCTGTTGAA	TGCAGTCCAA	ACATGAAAGG	4229
AAATAATTGT	TTTATATTAT	AACCTCTGAAG	CATGATAAAG	GGGCAGTTCA	CAATTTTCAC	4289
CATTTAAACA	CAAATTTGCT	GCACAGAATA	TCACCATTGC	AGTTCAAAAC	AAAACAAAAC	4349
AAAAAGTCTT	TTGTTTGTGA	ACACTGATGC	AAGAACTTGT	TTAAATGAAA	GGACTCTTTA	4409
CCCTAGAAGG	AAGAGGTGAA	GGATCTGGCT	TGTTTTTAAA	GCTTTATTTA	TTAAACCATA	4469
TTATTTGATT	ACTGTGTTAG	AATTTTCATAA	GCAATAATTA	AATGTGTCTT	TATGGAATTC	4529





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FIG. 5A

\*

CONS MARARPP.....s..11..1111dal...aa.pa.EvtLldskt.qgelGwishpp..Gwee.sg.den.tpirtYqCnvme.sqpn.WLrtnwi:  
EPH MERRWPLGLGLVLLLCAPLPPGARAKEVTLMDSKAQELGWLDDPKDGWSEQQILNGT.PLYMQDCPMQRRDTHWLRSNWIY  
ECK MELQAARACFALLWGCALAAAAAQAQKEVLLDFAAAGGELGWLTHPYCKGWLDMQNMNDM.PIYMSVCNVMMSGDDN.WLRTNWVY  
HEK4 MDCQLSILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQELGWI SYPSH.GWEEISGVDEHYTPRTYQVCNVMMDHSQNN.WLRTNWVP  
HEK5 LLAAVEETLMDSTTATAELGMMVHPPS.GWEEVSGYDENMNTIRTYQVCNVFESSQNN.WLRTKFIR  
HEK7 ALRTLLASPSNEVNLLDSRTVMGDLGWIAFPKN.GWEEIGEVDENYAPIHTYQVCVKMEQNQNN.WLLTSWIS  
HEK8 MAGIFYFALFSCFLGICDAVTGSRVYPANEVTLLDSRSVQELGWIASPLEGGWEEVSIIMDEKNTPIRTYQVCNVMPEPSQNN.WLRTDWIT  
HEK2 MARARPPPPPPGLPLPLPLPLPLLLPAGCRALHEETLMDTKWVTSALWTSHPES.GWEEVSGYDEAMNPRTYQVCNVRESSQNN.WLRTGFIW  
HEK11 MVFQTRYPSSIILCYIMLLRFAHTGEAQAKEVLLDLSKAQQTELEWISSPPN.GWEEISGLDENYTPRTYQVCQVMEPNQNN.WLRTNWIS

\*

\*

CONS rg.gaqriyvElkFt.RDCns.Pgvlgt..CKETFNlyyEsDdd....tgrniren.fvKidTiAaDesftq.Dlgdr.mklNtevsvGplskkGfYL  
EPH RGEASRVHVELQFTVRDCKSFPGGAGPLGCKKETFNLLYMESDQD...VGIQLRRPLFQKVTTVAADQSFTIRDLASGSVKLNVERCSLGRLTRGLYL  
ECK RG.EAERNNFELNFTVRDCNSFPGGASS..CKETFNLYYAESDLD...YGTNFQKRLFTKIDTIAPDEITVSSDFEARHVKLNVEERSVGPLTRKGFYL  
HEK4 RN.SAQKIYVELKFTLRDCNSIPLVLT..CKETFNLYYMESDLD...HGKVFREHQFTKIDTIAADESFTQMDLGDRLKLNTEIREVGPVNKKGFYL  
HEK5 RR.GAHRIVHEMKFSVRDCSSIPSVPGS..CKETFNLYYEAADFSAKTFFPNMENPWKVDTIAADESFQVDLGGVRMKINTEVRSFGPVSRSGFYL  
HEK7 NE.GASRIFIELKFTLRDCNSLPGGLGT..CKETFNMYEFESDDQ...NGRNKENQYIKIDTIAADESFTQMDLGDVRMKLNTEVRDVGPLSKKGFYL  
HEK8 RE.GAQRVYIEIKFTLRDCNSLPGVMT..CKETFNLYYVESDND...KERFIRENQVKIDTIAADESFTQVDIGDRIMKLNTEIRDVGPLSKKGFYL  
HEK2 RR.DVQRVVELKFTVRDCNSIPNIPS..CKETFNLFYEAADSDVASASSPFWMENPVKVDTIAPDESFSRLDAGR...NTKVRSFGLSKAGFY  
HEK11 KG.NAQRIFVELKFTLRDCNSLPGVLT..CKETFNLYYVETDYD...TGRNIRENLYVKIDTIAADESFTQDGLGERMKLNTEVREIGPLSKQKGFYL



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BY	CLASS
DRAFTSMAN	SUBCLASS

FIG. 5B

\* \* \* \* \*

CONS AFqdvGaC.aLvsVrv.ykkCpstv.nLA.Fpdr.tgadsssLvevrG.Cvna....e...pp.m.CsadGEWlVPiGkC.CkaGyee...gtaCqaCp

EPH AFHNPgACVALSVRVFYQRCPETLNGLAQFPDTLPg.PA.GLVEVAGTCLPHARASPRPSGAPRMHCSPDGEWLVPVGRCHCEPGYEEGSGEACVACP

ECK AFQDIGACVALLSVRVYKKCPPELLQGLAHFPETIAGSDAPSLATVAGTCVDHA.VVPPGEEPRMHCAVDGEWLVPiGQCLCQAGYEKVED..ACQACS

HEK4 AFQDVGACVALSVRVFYKKCPFTVKNLAMPDTPV.MDSQSLVEVRGSCVNNs...KEEDPPRMYSCTEGEWLVPiGKCSNAGYEER..GFMCQACR

HEK5 AFQDYGGCMsLIAVRVfYRKCPRiIQNGAIFQETLSGAESTSLVAARGSCIANA...EEVDVPIKLYCNGDGEWLVPiGRMCCKAGFEAVENGTVCRGCP

HEK7 AFQDVGACIALSVRVYKKCPVVRHLAVFPDTITGADSSQLLEVSGSCVNNs...VTDEPPKMHCsAEGEWLVPiGKCMCKAGYEER.NGT.CQVCR

HEK8 AFQDVGACIALSVRVYKKCPPLTVRNLAQFPDTITGADTSSLVEVRGSCVNNs...EEKDVPKMYCGADGEWLVPiGNCLCNAGHEER..SGECQACK

HEK2 AFQDQGACMSLISVRAFYKKCASTAGFALFPETLTGAETSLVIAPGTCPNA...VEVSVPKLYCNGDGEWMPVVGACTCATGHEPAAKESQCRPCP

HEK11 AFQDVGACIALSVKVYKKCWSIIENLAIFPDTVTGSEFSSLVEVRGTCVSSA...EEEEANAPRMHCsAEGEWLVPiGKICKAGYQK..GDTCEPCG

\* \* \* \* \*

CONS pGfyka..gd.pClkCPpHs.ttsegatsCtCengy.RadsdppsmaCTrpPSaPrnlisnvnetsv.LewspPadtGgR.Dv.yn.iCkkCg.ga...g

EPH SgsYRMDMDTPHCLTCpQQSTAESEGATICtCESGHYRAPGEGPQVACTGPPSAPRNLSPSASGTQLSLRWEPPADTGRQDVRYSVRCSQCQGTADGG

ECK PGFFKFEASESPCLEPEHTLPSPEGATSCeCEEGFFRAPQDPASMPCTRPSPAPHYLTAUGMGAKVELRWTPPDQSGGREDIVYSVTCEQCWPES...G

HEK4 PGFYKALDGNMKCAKCPHsSTQEDGSMNCRCENNYFRADKDPpSMACTRPPSSPRNVISNINETSvILDWSWPLDTGGRKDVTFNIICKKGWNI...

HEK5 SGTFFKANQGEACTHCPINSRTTSEGATNCVRNGYRADLDPLDMPCTTIPSAQAVISSVNETSMLWTPPRDSSGGREDLVNLIICKSCGSGR...

HEK7 PGFFKASPHIQSCGKCPHsYTHEEASTSCVCEKDYFRRESDPPTWACTRPSPAPRNAISNVNETSvFLEWIPADTGRKDVSYVIACKKCNsha...

HEK8 IGYKALSTDATCAKCPHsYSVWEGATSCtCDRGFFRADNDAAAMPCTRPSPAPLNLIISNVNETSvNLEWSSPQNTGGRQDISYNVVKKCGAGD...P

HEK2 PGsYKAKQGEPCPLPCPPNSRTTSPAAStCTCHNNFYRADSDSADsACTTVPSPPRGVIsNVNETSvLLEWSEPRDLGVRDdLLYNVICKKc.HGAGGA

HEK11 RGFYKSSSQDLQCSRCPHsFSDKEGSSRCECEDGYRAPSDPPYVACTRPSPAPQNLIFNINQTTVSLEWSPPADNGGRNDVTYRILCKRCSWEQ...

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FIG. 5C

\* \*

CONS .CepCg.nvry.prglgt.t.vtvsdllahtnYtFe.eAvNGVs.l.....sp.q.asvsv.ittnqaaps.v.tvr.....sr.s.slsW.qep.rpngv  
EPH PCQPCGVGHFSPGARALTTPAVHNGLEPYANYTFNVEAQNGVSGLGSSGHAS..TSVSISMGHAESLS..GLSLRLVKKEPRQLELTWAGSRPRSPGA  
ECK ECGPCEASVRYSEPPHGLTRTSVTVSDLEPHMNYTFTVEARNGVSGLVTSRFR.TASVS..I..NQ...TEPPKVRLEGRSTTSLSVSW.SIPPPQQR  
HEK4 QCEPCSPNVRLPRQFGLTNTTVTVDLLAHTNYTFEIDA VNGVSEL..SSPPRQFAAV..SITTNQAAPSPVLTIKKDRTSRNSISLSW.QEPEHPNGI  
HEK5 ACTRCGDNVQYAPRQLGLEPRTIYISDILLAHTQYTFEIQAVNGVTD..QSPFSPQFASV..NITTNQAAPSAVSIMHQVSRVTVDISITLSW.SQPDQPNGV  
HEK7 VCEECGGHVRYLPRQSGLKNTSVMVDDL AHTNYTFEIEAVNGVSDL....SPGARQYVSVNVTNQAAPSPVTNVKKGIAKNSISLSW.QEPDRPNGI  
HEK8 KCRPCGSGVHYTPQONGKLTTKVSITDILLAHTNYTFEIWA VNGVSK....YNPNPDQSVSVTNTNQAAPSSIALVQAKEVTRYSVALLAW.LEPDRPNGV  
HEK2 ACSRCDDNVEFVPRQLGLEPRVHTSHLLAHTRYTFEVQAVNGVSGK....SPLPPRYAAVNITTNQAAPSEVPTLRLHSSSGSLTSLW.APPERPNGV  
HEK11 ECVPCGSGNIGYMPQQTGLEDNVYTVMDLLAHANYTFEVEAVNGVSDL....SRSQRLFAAVSITTGQAAPSQVSGVMKERVLRQSVLSW.QEPEHPNGV

CONS il.YEVkyyekdq.ersy.iv.k.tsvt.dgLkpdT.YvfqvrarTaaGyG..Sr..efeP.pea.sgsG...ivvviivs.aga..llvw..v.l..r  
EPH NLTYE....LHVLNQDEERYQMVL EPRVLLTELQPDTTYIVRVRLM TPLGPGFSPDHEFRTPPVSRGLTGGEIVAVIFGLLLGAALLGILVFRSRRRA  
ECK VWKYEV.TYRKKGDSNSYNVRTEGFSVTLDLAPDTTYLVQVQALTQEGQGAGSKVHEFQTLSPGSGNLAVIGGVAVGVVLLLVLAGVGVFFIHRRRKN  
HEK4 ILDYEVKYEKQEQETSYTILRAGTNVTISSLKPDITYVLQIRARTAAGYGTNSRKFETSPDSFSISGESSQVVMIAISA AVAILLTWVIVVLIGR  
HEK5 ILDYELQYKEKELSEYNATAIKSPNTNTTVQGLKAGAIYVFQVRARTVAGYGRYCKMYFTMTAEYQTSIQEKLPLIIGSSAAGLVFLIAVWVIAIVC  
HEK7 ILEYEIKHFEDQETSYTII.KSKETTITAEGCLKPASVYVFQIRARTAAGYGVFSRRFEFETTPVFAASSDQSQIPVIAVSVTVGVILLAWIGVLLSGR  
HEK8 ILEYEVKYEKDQNERSYRIVRTAARNTDIKGLNPLTSYVFHVRARTAAGYGVDFSEPLEVTNTVPSRIIGDGANSTVLLVSVSGSVLVVILIAAFVIS  
HEK2 ILDYEMKYFEK..SEGIASVTQSMNSVQLDGLRPDARYVQVRARTVAGYGVQYSRPAEFETTSERGSAQQLQEQPLIVGSATAGLVFWVAVVIAIV  
HEK11 ITEYEIKYYEKDQRERTYSTVTKTKSTASINNLKPGTVYVFQIRAFRTAAGYGNYSPLDVTATLEATGKMFEATVSSEQNPVILIAVXVAGTIIILVFM

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	DAFFMAN		

FIG. 5D

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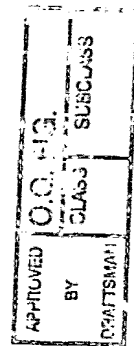
CONS .r..qsr.dd.ey.keq.....klpg.ktyidP.TyedPnqav.efakEidascikiekViGaGEFGEVcsGrLklp.gkre..VAIKTLKvgY  
EPH QRQRQRHVTA PPMWIERTSCAALCGTSRHTRTLHREPWTL..PGGWSNFPSPRELDPAWLMVDTVIGEGEFGEVYRGTLRLPS.QDCKTVAIKTLKDTs  
ECK QRARQSPEDVYFSKSEQ.....LKPLKTYVDPHTYEDPNQAVLKFTEIHPSCVTRQKVI GAGEFGEVYKGM LKTSsGKKEVPVAIKTLKAGY  
HEK4 FCGYKSKHGADKRLHFGNG.....HLKPLGLRTYVDPHTYEDPTQAVHEFAKELDATNISIDKVVGAGEFGEVCSGRLKLPs.KKEISVAIKTLKVGy  
HEK5 NRRGFERADSEYTDKLQHYT.....SGHITPGMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLP.GKREIFVAIKTLKSGY  
HEK7 RCGYSKAKQDPEEEKMHFN.....GHIKLPGVRTYIDPHTYEDPNQAVHEFAKEIEASCITIERVIGAGEFGEVCSGRLKLP.GKRELPAIKTLKVGy  
HEK8 RRRSKYSKAKQEADEEKHLN.....QGVRTYVDPFTYEDPNQAVREFAKEIDASCIEKIEKVIGGEFGEVCSGRLKVP.GKREICVAIKTLKAGY  
HEK2 CLRKQRHGSDSSEYTEKLQOY.....IAPGMKVYIDPFTYEDPNEAVREFAKEIDVSCVKEIEVIGAGEFGEVCRGRLKQP.GRREVFVAIKTLKVGy  
HEK11 VFGFIIGRRHCGYTKADQEGDEELYFHFKPGTKTYIDPETYEDPNRAVHQFAKELDASCIEKIERVIGAGEFGEVCSGRLKLP.GKRDVAVAIKTLKVGy

CONS tekQrrdFL.EASIMGQFdHpniihLEGVvtkskPvMIite.MENG.Ld.FLrknDgqftviQLVgMLrGlaaGMkVlsdmYVHRDLAARNILvNsNLv  
EPH PGGQWwNfLREATIMGQFSHPHILHLEGVvTKRKPIMIITEFMENAALDAFLREREDQLVPGQLVAMLQGIASGMNVL SNHNYVHRDLAARNILVNQNLc  
ECK TEKQRVDFLGEAGIMGQFSHHNIIRLEGVISKYKPMMIITEYMENGALDKFLREKDGESVLQLVgMLRGIAAGMKVLANMNYVHRDLAARNILVNSNLV  
HEK4 TEKQRRDFLGEASIMGQFDHPNIIRLEGVvTKSKPVMIVTEYMENGSLDSFLRKHDAQFTVIQLVgMLRGIAAGMKVLSDMGYVHRDLAARNILINSNLV  
HEK5 TEKQRRDFLSEASIMGQFDHPNVIHLEGVvTKSTPVMIIITEFMENGSLDSFLRQNDGQFTVIQLVgMLRGIAAGMKVLA DMNYYVHRDLAARNILVNSNLV  
HEK7 TEKQRRDFLGEASIMGQFDHPNIIHLEGVvTKSKPVMIVTEYMENGSLDTFLKNDGQFTVIQLVgMLRGISAGMKVLSDMGYVHRDLAARNILINSNLV  
HEK8 TDQRRDFLSEASIMGQFDHPNIIHLEGVvTKCKPVMIIITEYMENGSLDAFLRKNDRFTVIQLVgMLRGISGMKVLSDMSYVHRDLAARNILVNSNLV  
HEK2 TERQRRDFLSEASIMGQFDHPNIIIRLEGVvTKSRPVMIIITEFMENCALDSFLRLNDGQFTVIQLVgMLRGIAAGMKVLS EMMYVHRDLAARNILVNSNLV  
HEK11 TEKQRRDFLCEASIMGQFDHPNVVHLEGVvTRGKPMIVIEFMENGALHAFLRKHGQFTVIQLVgMLRGIAAGMRVLA DMGYVHRDLAARNILVNSNLV

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# FIG. 5E

\*  
CONS CKVSDFGLSRVLEDD.pea.yt.trGGKiPIrWTaPEAIaYrkFTsASDVWSyGIVmWEVmsyGerPYw.msNqdVikaieegyRLPpPmDCPaal.qLM  
EPH CKVSDFGLTRLL.DDFDGTyET..QGGKiPIrWTaPEAIaHRIFTTASDVWSFGIVmWEVLSFGDKPYGEMSNQEVmKSIEDGYRLPPPVDCPaPLYELM  
ECK CKVSDFGLSRVLEDD.PEAyT.TSGGKiPIrWTaPEAIaYrkFTsASDVWSFGIVmWEVmsyGerPYwELSNHEVMKAINDGFRLLPTPMDCPsAIYQLM  
HEK4 CKVSDFGLSRVLEDD.PEAyT.TSGGKiPIrWTsPEAIaYrkFTsASDVWSyGIVLWEVmsyGerPYwEMSNQDVikaVDEGYRLPPPMDCPaALYQLM  
HEK5 CKVSDFGLSRFLEDDTSDPTyTSALGGKPiRWTaPEAIQYrkFTsASDVWSyGIVmWEVmsyGerPYwDMTNQDVINAIEQDYRLPPPMDCPaSALHQLM  
HEK7 CKVSDFGLSRVLEDD.PEAyT.TSGGKiPIrWTaPEAIaYrkFTsASDVWSyGIVmWEVmsyGerPYwEMTNQDVikaVEEGYRLPSPMDCPaALYQLM  
HEK8 CKVSDFGMSRVLEDD.PEAyT.TSGGKiPIrWTaPEAIaYrkFTsASDVWSyGIVmWEVmsyGerPYwDMSNQDVikaIEEGYRLPPPMDCPiALHQLM  
HEK2 CKVSDFGLSRFLEDDPSDPTyTSSLGGKPiRWTaPEAIaYrkFTsASDVWSyGIVmWEVmsyGerPYwDMSNQDVINAIEQDYRLPPPMDCPaTALHQLM  
HEK11 CKVSDFGLSRVLEDD.PEAyT.TTGGKiPVRWTaPEAIQYrkFTsASDVWSyGIVmWEVmsyGerPYwDMSNQDVikaIEEGYRLPAPMDCPaGLHQLM  
\*  
\*  
CONS ldcWqk.RnrRpKf.qivnildkIrnPNsLktia.assr.s.plld.sgpD.ttfrtvgeWLeaikmgryke.Ftaagyts..avaqmtaEdl.rIGvt  
EPH KNCWAYDRARRPHFQKLQAHLEQLLANPHSLRTIANFDPRVTLRLPSLSGSDGIPYRTVSEWLEsIRMKRYILHFHSAGLDTMECVLELTAEDLTQMGIT  
ECK MQCWQqERARRPKFADIVSILDKLIRAPDSLKTlADFDPRVSIrLPSTSGSEGVPFRTVSEWLEsIKMQQYTEHFMAAGYTAIEKVvQMTNDDIKRIGVR  
HEK4 LDCWQKDRNRRPKFEQIVSILDKLIRNPGSLKIITSAAARPSNLLLDQSNVDISTFRttGDWLNgrVrTAHCKEIFTGVEYSSCDTIaKISTDDMKKVGVT  
HEK5 LDCWQKDRNRRPKFGQIVNTLDKMIRNPNsLKAMAPLSSGINPLLDRTIPDYTSFNTVDENLEAIKMGQYKESFANAGFTSFDFVSQMMEDILRVGVT  
HEK7 LDCWQKERNsRPKfDEIVNMLDKLIRNPSSLKTLVNAsCRVSNLLAEHSPLGSGAYRSVGEWLEAIKMGRYTEIFMENGYSMDAVAQVtLEDLRLRGVT  
HEK8 LDCWQKERSDRPKFGQIVNMLDKLIRNPNsLKRTGTESsRPNTALLDPSSPEFSaVVSVDWlQAIKMDRYKDNFTTAAGYTTLEAVHVNQEDLARIGIT  
HEK2 LDCWVRDRNLRPKFSQIVNTLDKLIrNAASLKVIAAQSGMSQPLLDRTVPDYTTFTTVGDWLDaIKMGRYKESFVSAGFASFDLVAQMTAEDLLRIGVT  
HEK11 LDCWQKERAERPKEQIVGILDKMIRNPNsLKTPLGTCsRPIsPLLDQNTPDFTTFCsVGEWlQAIKMERyKDNFTTAAGYNSLESVARMTIEDVMSLGIT



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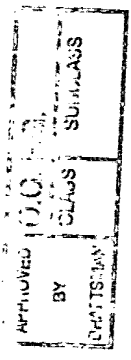


FIG. 5F

CONS	lvghQkklslsq.mr.Qmnggh.p.v.v
EPH	LPGHQKRILCSIQGFKD
ECK	LPGHQKRIAYSLGLKQDVNTVGIP
HEK4	VGPQKKIISIKALETQSKNGPVPV
HEK5	LAGHQKKILNSIQVMRAQMNQIQSVEV
HEK7	LVGHQKKIMNSLQEMKVQLVNGMVPL
HEK8	AITHQNKILSSVQAMRTQMOMHGRMPV
HEK2	LAGHQKKILSSIQDMRLQMNQTLVPQV
HEK11	LVGHQKKIMSSIQTMRQAQMLHLHGTGIQV



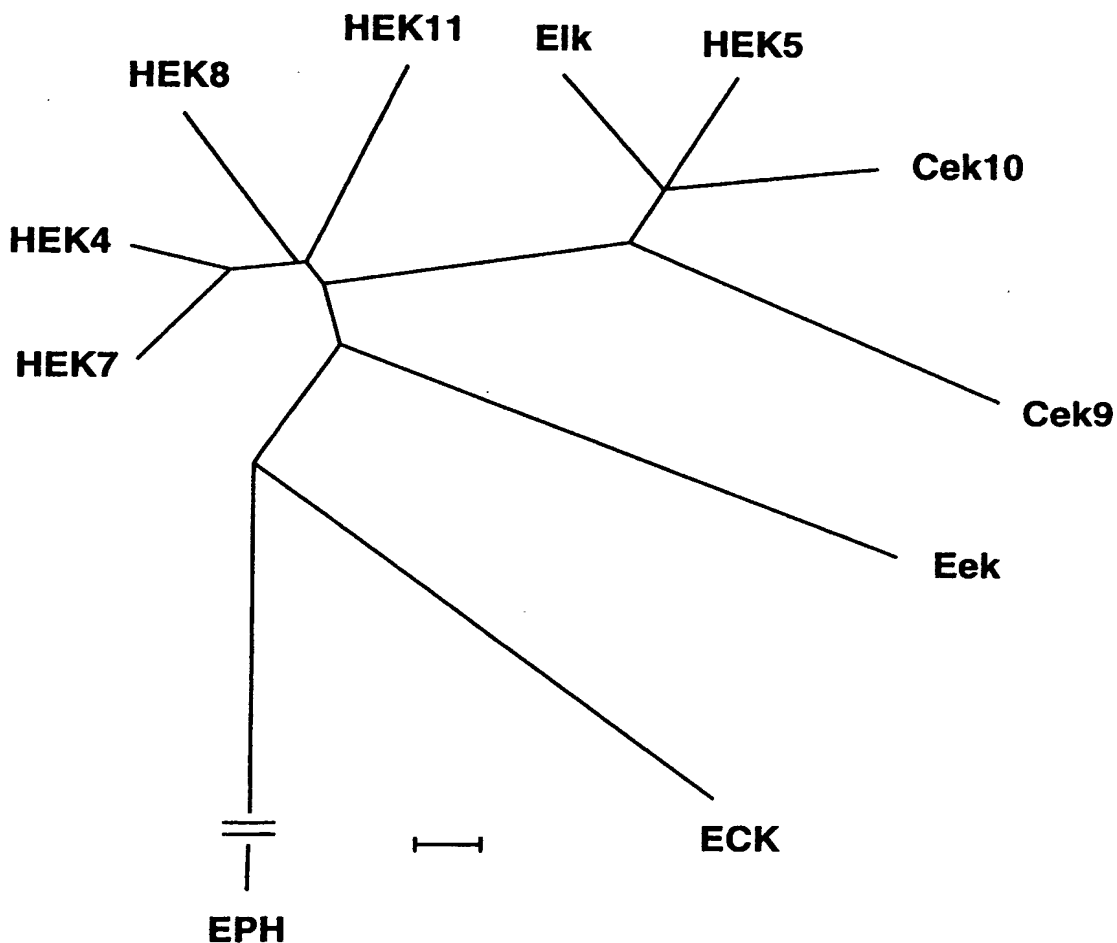
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**FIG. 6**

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DRAFTSMAN		





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FIG. 7A

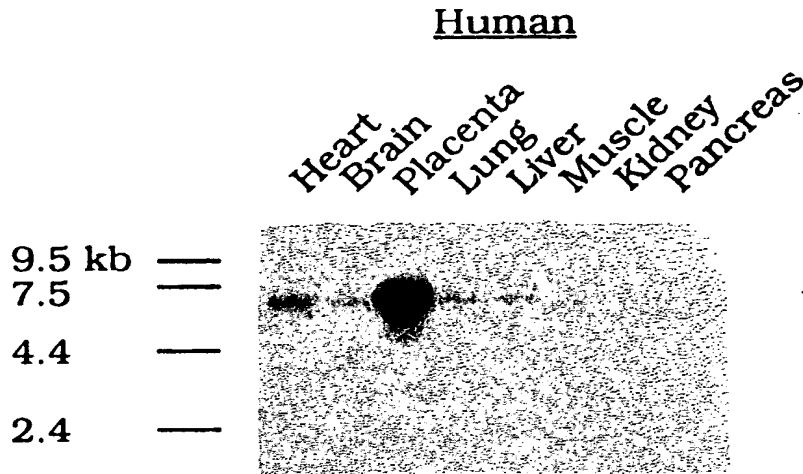
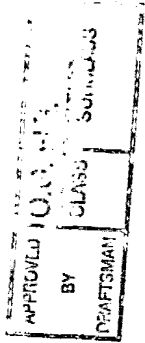
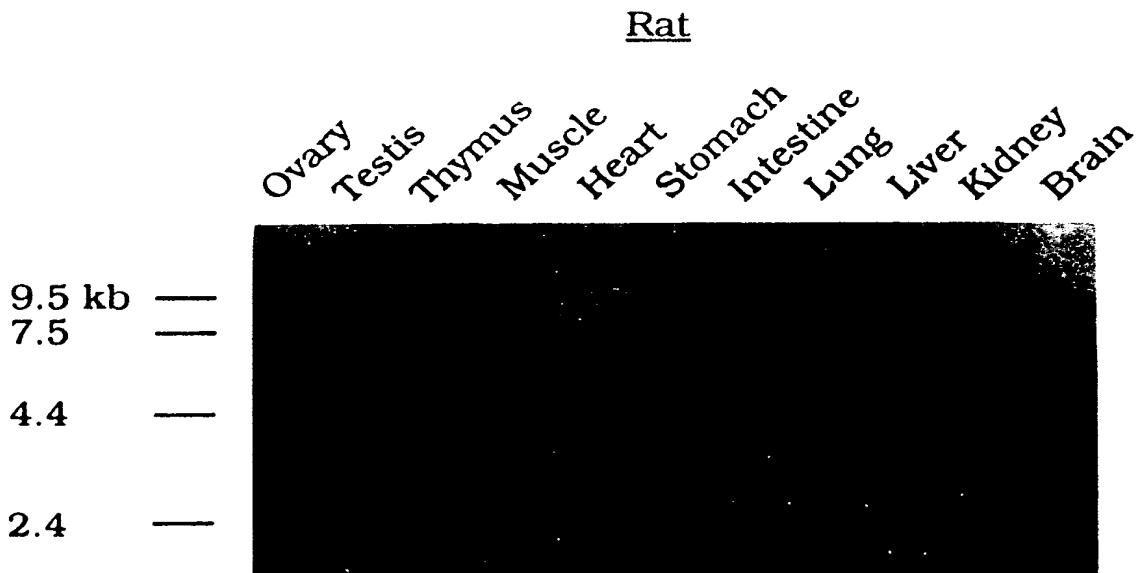


FIG. 7B





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FIG. 8A

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APPROVED BY DRAFTSMAN	O.G. FIG.	SUBCLASS
	CLASS	

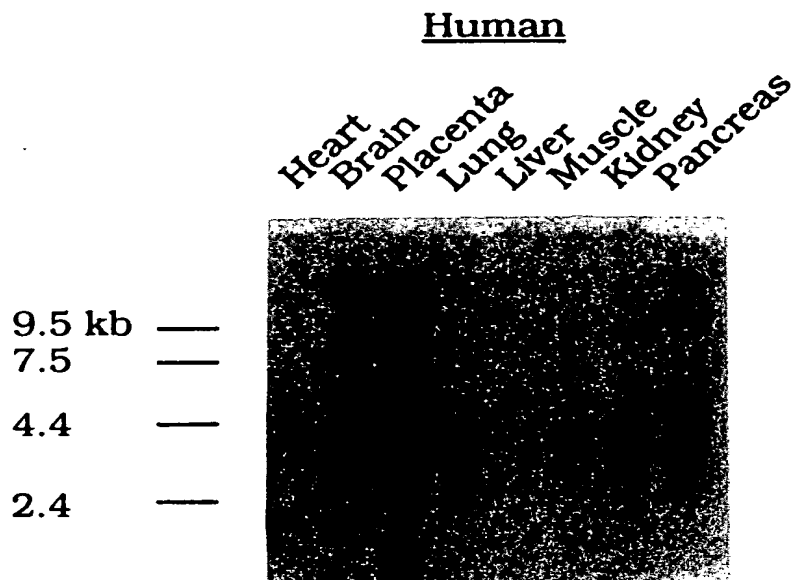
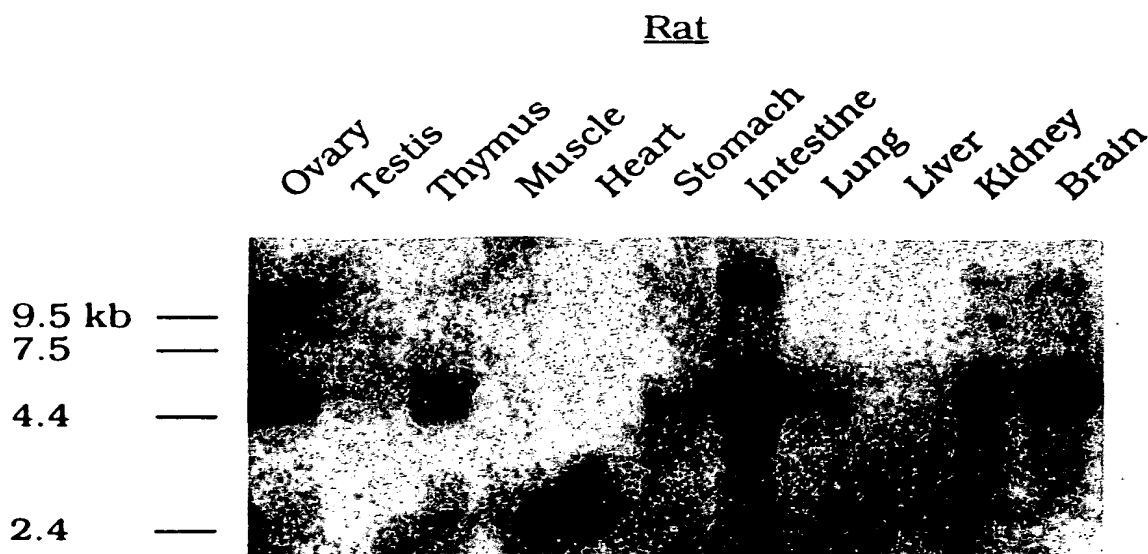


FIG. 8B





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FIG. 9A

Human

Heart  
Brain  
Placenta  
Lung  
Liver  
Muscle  
Kidney  
Pancreas

9.5 kb —  
7.5 —  
4.4 —



FIG. 9B

Rat

Ovary  
Testis  
Thymus  
Muscle  
Heart  
Stomach  
Intestine  
Lung  
Liver  
Kidney  
Brain

9.5 kb —  
7.5 —  
4.4 —





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FIG. 10A

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APPROVED	CLASS	SUBCLASS
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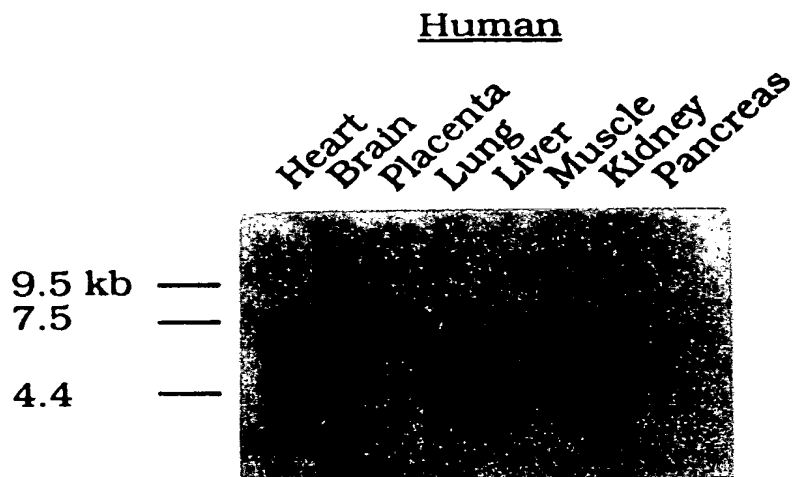
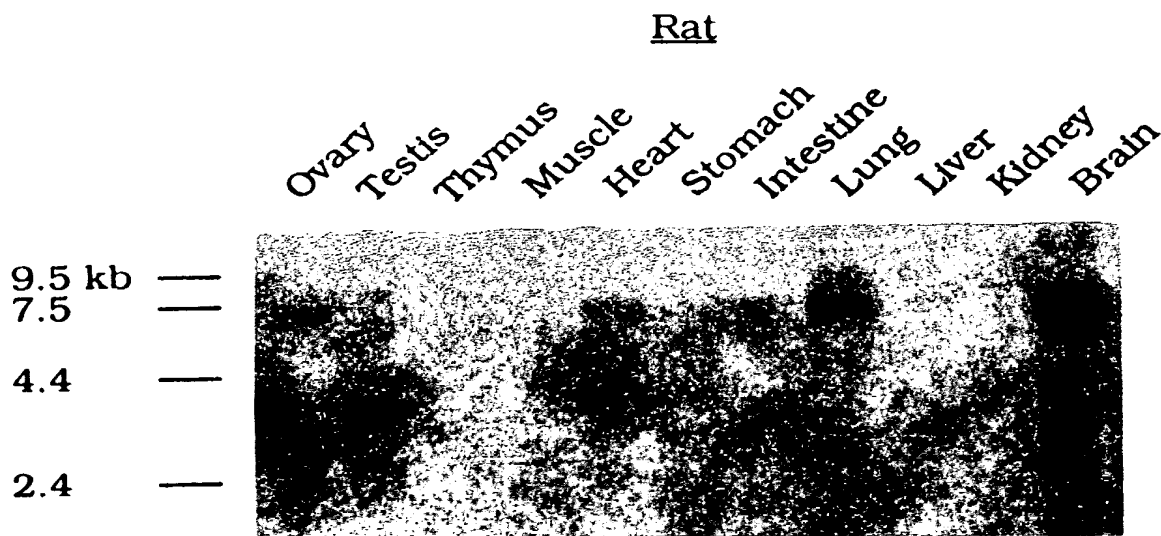


FIG. 10B







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FIG. 11A

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APPROVED BY DRAFTSMAN	CLASS	SUBCLASS
	O.G. FIG.	

Human

Heart  
Brain  
Placenta  
Lung  
Liver  
Muscle  
Kidney  
Pancreas

9.5 kb —  
7.5 —  
4.4 —  
2.4 —

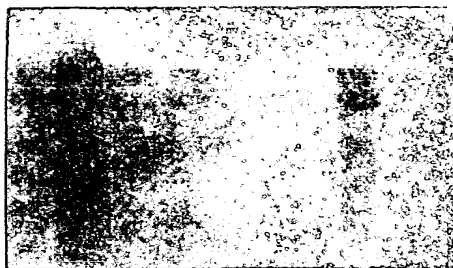


FIG. 11B

Rat

Ovary  
Testis  
Thymus  
Muscle  
Heart  
Stomach  
Intestine  
Lung  
Liver  
Kidney  
Brain

9.5 kb —  
7.5 —  
4.4 —  
2.4 —

